

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 169483

TO: David Lukton

Location: rem/3B75/3C18

Art Unit: 1654 (<u>Art 26</u>, 2005

Case Serial Number: 10/014147

From: P. Sheppard

**Location: Remsen Building** 

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes	
•	

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SEAL	RCH REQUEST FORM (STIC)	10/25/05	ME
Requestor's Name: David Lukton	Examiner number: 71263	Date:	
	İ	10-014147	

Art Unit: 1654 Phone number: 571-272-0952 Serial Number:

Mail Box: 3-C-18 Examiner Rm: 3-B-75 Results format: paper

Title: SYNTHETIC PEPTIDES THAT INHIBIT LEUKOCYTE SUPEROXIDE ANION PRODUCTION AND/OR ATTRACT LEUKOCYTES

Applicants: BLECHA, FRANK; SHI, JISHU

Earliest Priority Date: 4/10/95

Please search SEQ ID NOS: 1, 2, 5, 6, and 7

RECEIVED

OCT 25 2005

ECHIVCHEN DIVISION
(STIC)

**********	***********	***********
STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher:	NA Sequence (#)	STNDialog
Searcher Phone #:	AA Sequence (#)	Questel/Orbit Lexis/Nexis
Searcher Location:	Structure (#)	Westlaw WWW/Internet
Date Searcher Picked Up:	Bibliographic	In-house sequence systems
Date Completed:		Commercial Oligomer Score/Length SPDI Encode/Transl Other (specify)
Online Time:	Other	•

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

October 26, 2005, 04:51:43 ; Search time 153.518 Seconds (without alignments) 98.253 Million cell updates/sec

US-10-014-147-1 score: Title: Perfect

238 1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFP 39 Sequence:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Searched:

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\*

11. geneseq1980s:\*

22. geneseq1980s:\*

33. geneseq200s:\*

43. geneseq2001s:\*

55. geneseq201s:\*

66. geneseq20303as:\*

77. geneseq2033as:\* Database

geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	-		Aar94446 Synducin			•			•				_			Aaw75723 Proline/A		Adl67255 Antimicro		Ade86114 Proline-a	-		S	Adl67257 Antimicro	Abo57093 Human gen
SOFTWANTES	QI	AAR30491	AAR99121	AAR94446	AAW01446	AAW75722	AAB26888	AAB97280	AAB84690	ADD35364	ADE86112	ADL67254	ABB07714	ADR82250	AAB51194	AAW01447	AAW75723	ADE86113	ADL67255	AAW01451	ADE86114	ADL67256	AAW01452	ADE86115	ADL67257	ABO57093
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٠	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	.100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	65.1	65.1	65.1	65.1	58.8	58.8	œ	48.7	48.7	48.7	44.1
	Score	238	238	238	238	238	238	238	238	238	238	238	238	238	238	155	155	155	155	140	140	140	116	.116	116	105
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu20105 Protein e Aag38942 Arabidops Aay67470 Np70 prot Aay17387 Human DNA	000000	Aab47514 NpwBP 12 Abo53032 Human put Ade59851 Human Pro Aab53462 Human Col Aar82569 Pig leuko Aar82562 Pig leuko	Pig Pig Huma Prop
ABU20105 AAG38942 AAY67470 AAY17387	ADE59849 ABB66956 AAY67469 AAY82327 AAY72165	AAB47514 ABC53032 AAB59851 AAB53462 AAR82569	AAR82566 AAR82564 ADC87385 AAU56017 ABMS2536
9 7 7 7	174664	407820	100740
205 763 250 311	389 502 641 641	641 641 647 79	649 143 143
443.1 42.6 42.6	44444 100000 000000	4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6
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#### ALIGNMENTS

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This peptide was isolated from the small intestine of a pig. The small instine is an important endocrine organ and many physiologically active peptides have been isolated from it. This peptide inhibits the growth of, and may kill, bacteria, pref. gram negative bacteria. This peptide or its functional derivatives may be used in human or veterinary medicine for the perpetic or prophylactic use. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                               New anti-bacterial polypeptide - active against Gram negative bacteria.
                                                                                                                             Pig; small intestine; endocrine; gram negative; bacteria; therapeutic; veterinary medicine; prophylactic.
                                                                                                                                                                                                                                                                                                                                                  Joernvall H;
                     AAR30491 standard; peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 10; 15pp; English.
                                                                                                                                                                                                                                          92WO-SE000394.
                                                                                                                                                                                                                                                                  91SE-00001838.
                                                                                                                                                                                                                                                                                                                                                   Boman HG, Mutt V,
                                                                     (revised)
(first entry)
                                                                                                         Antibacterial peptide.
                                                                                                                                                                   Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                           JOERNVALL H.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-018080/02
                                                                                                                                                                                                                                                                                         LEE J.
BOMAN H G.
                                                                                                                                                                                            W09222578-A1.
                                                                                                                                                                                                                                          10-JUN-1992;
                                                                                                                                                                                                                                                                14-JUN-1991;
                                                                                                                                                                                                                   23-DEC-1992.
                                                                     25-MAR-2003
12-MAY-1993
                                              AAR30491;
                                                                                                                                                                                                                                                                                        (LEEJ/) 1
(BOMA/) 1
(MUTT/) 1
(JOER/) 5
                                                                                                                                                                                                                                                                                                                                                     Lee J,
RESULT 1
           AAR30491
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Sequence 39 AA;

Query Match

100.0%; Score 238; DB 2; Length 39;

Matches

AAR9912

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The present peptide is a synducin, which induces the expression of syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp. fibroblasts and epithelial cells. The 36 N-terminal amino acids of the peptide were found to be identical to the 36 N-terminal amino acids of PR -39, a Pro and Arg rich antibacterial peptide previously found in porcine intestine (W09222578). Synducins may be used in the treatment of stasis and decubitus ulcers, keloids, skin burns, ischemic tissues and hypercoagulation states, prevention of tumour metastasis, restenosis inhibition and endothelial cell angiogenesis and proliferation induction. Human microvascular endothelial cells were assayed for syndecan-4 expression following exposure to 5 % wound fluid, dbcAMP (1 mM), the present peptide (10 microM) or a blank, to give respective cell surface syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating mesenchymal interaction by administration of synducin - used
                                                                                                                         Synducin; induction; expression; syndecan-1; syndecan-4; surface; mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis; decubitus; ulcers; keloids; skin burns; ischemic tissues; hypercoagulation states; prevention; tumour metastasis; restenosis; inhibition; angiogenesis; proliferation; endothelial.
                                                                                    Synducin peptide (PR-39) induces syndecan expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the treatment of wounds, tumours, restenosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW01446 standard; peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 26; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US012080.
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                                       05-NOV-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallo RL, Bernfield M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-188401/19.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1994;
                                                                                                                                                                                                                                                                                                           WO9609322-A2
                                                                                                                                                                                                                                                                                                                                                          28-MAR-1996.
                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by administering magainin antimicrobial or squalamine cpd. to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                            STD; sexually transmitted disease; HIV; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 herpes simplex virus; HSV; Neisseria gonnorhoeae; Candida; Chlamydia;
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
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                     Pred. No. 2.7e-15;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33
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                                                                                                                       1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFP
                                                                                      1 RRRPRPPYLPRPPPFFPPRLPPRIPPGFPPRFPPRFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           magainin; antimicrobial; squalamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacob L, Zasloff M, Williams T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 32; 60pp; English.
                                                                                                                                                                                                                                              AAR99121 standard; peptide; 39 AA
100.08; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAGA-) MAGAININ PHARM INC
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Conservative
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-179725/18.
                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9608270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                             AAR99121;
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                                                                                                                                                                                                                                                                                                                            Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig antimicrobial peptide; small intestine; human; neutrophil; bacteria; DNA synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
                                  Gaps
                                    .;
0
Length 39;
                                    Indels
                                                                    1 RRRPRPPYLPRPPPFFPPRLPPRIPPGFPPRFP
                                                                                          RRRPRPYLPRPRPPFPPRLPPRIPPGFPPRFPPRFP
 DB 2;
 100.0%; Score 238; DB 2; 100.0%; Pred. No. 2.7e-15;
                                                                                                                                                                                                                                                                                              Leukocyte 02- production inhibitor peptide PR39.
                                    0; Mismatches
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AAR94446 standard; peptide; 39 AA.

RESULT 3

Matches

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AAR9446;

Synthetic.

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This sequence represents the proline-arginine rich antimicrobial peptide PR39. The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophila. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. This sequence, and the fragments of it shown in AAW01447-W01454, can be used in the method of the invention. The method of the invention is for inhibiting leukcyte superoxide anion (O2-b) production. The method compairs a daministering to a leukcyte a peptide (such as this sequence) capable of inhibiting leukcyte 02- production. The peptides can be used as medicaments for fighting infection by attracting leukcytes to a wound site and restricting infection by these the wound site caused by excessive oxygen radicals produced by these leukcytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
                                                                                                                                                                                                                                                    Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 2.7e-15;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proline/Arginine rich peptide PR-39
                                                                                                                                                         (UNIV ) UNIV KANSAS STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW75722 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                      Claim 2; Page 26; 45pp; English.
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                                                                                           96WO-US004674
                                                                                                                          95US-00419066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                       WPI; 1996-476842/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9835690-A1
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16-FEB-1998;
                                                                                           10-APR-1996;
                                                                                                                           .0-APR-1995;
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                              WO9632129-A1
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                                                            17-0CT-1996
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                                                                                                                                                                                         Blecha F,
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Gaps

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Sequences AAW75722-W75732 are proline/arginine rich peptides that upon administration into a mammal's bloodstream reduce reperfusion injury cadministration into a mammal's bloodstream reduce reperfusion injury (production of reactive oxygen species, neutrophils adherence to condotherlium, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXF, where P is a condition residue and X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was cetablished by structural and function analysis that a peptide should contain 4 or 6 of these motifs, and that inhibitory activity is correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the neutrophil superoxide anion, and also the inhibition of neutrophil superoxide anion, and also the inhibition of neutrophil condasse to some extent. All of the peptides also inhibit neutrophil oxidase activity. PR-39 is believed, to be the most potent endogenous down regulator of NADPH oxidase yet discovered, and from the data conduction inhiny inhinced advanced in eliminating or reducing the reperfusion inhiny inhinced advanced in calminating or reducing the reperfusion inhiny indired advanced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the reperfusion injury induced adhesion and extraction of neutrophils. The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery
                                                                                                        Reduction of reperfusion injury in temporarily occluded blood vessels by administration of a peptide which is rich in proline or arginine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction; myocardial ischaemia; proteasome.
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100.0%; Pred. No. 2.7e-15;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR-39 peptide used in angiogenesis control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                (UNIV ) UNIV KANSAS STATE RES FOUND.
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                                                                                                                                                                                                           Claim 3; Page 14; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000; 2000WO-US007050.
                                                     Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Matches 39; Conservative
                                                     Blecha F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39 AA;
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                                                       Ross CR,
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Gao Y;

Simons M,

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Matches
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                                                                                                           This invention relates to a method for the stimulation of angiogenesis in situ within a targeted collection of viable cells. The method comprises introducing, into the cytoplasm, at least 1 member of the PR-39 oligopeptide collective, which interacts with cytoplasmic proteasomes. Part of the proteolytic activity of the proteosomes is selectively angiogenesis. The method is used to induce angiogenesis in tissue that has suffered anoxia or infarction, e.g. myocardial infarction or chronic myocardial ischaemia, and also to study the mechanisms that control angiogenesis. The present sequence represents the PR-39 peptide from which peptide used in the method of the invention are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stimulation of angiogenesis and inhibition of proteasome mediated degradation in cells, by introduction of PR-39 oligopeptide or its N-terminal fragments or their conjugates, for use in anoxia and infarction
                          Stimulating angiogenesis in situ, useful e.g. for treating anoxia and infarction, by administering a PR-39 oligopeptide that regulates enzymatic activity of proteosomes.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR-39; cathelin; inflammation; wound healing; myocardial infarction; proteasome; proteolysis; alpha7; peptide degradation; angiogenesis; anoxia; chronic myocardial ischaemia; heart tissue.
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                                                                                                                                                                                                                                                                                                             100.0%; Score 238; DB 3; Length 39; 100.0%; Pred. No. 2.7e-15; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 21; 52pp; English.
                                                                                   Disclosure; Page 21; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB97280 standard; peptide; 39 AA
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                                                                                                                                                                                                                                                                                                                             Similarity 100.
39; Conservative
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WPI; 2000-628319/60.
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                                                                                                                                                                                                                                                                                    Sequence 39 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR-39 peptide.
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Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39 is a member of the the cathelin family of proteins, mature PR-39 represented by the present sequence is 39 amino acids in length, and has been shown to play a role in several inflammatory events including wound healing and myocardial infarction. The PR-39 derived family of

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oligopeptides cause selective inhibition of proteasome mediated degeneration of peptides and stimulation of angiogenesis after their intracellular introduction to a target cell. PR-39 derived peptides are able to interact with at least the alpha7 subunit of the proteasomes, and therefore alter the proteolytic activity of proteasomes such that a selective increased expression of specific proteins occurs. The invention includes methods for the selective inhibition of proteasome mediated peptide degradation. The method provides means for stimulating angiogenesis as required in living tissues and organs which have suffered of chronic myocardial ischaemia of heart tissue. Examples are the myocardial ischaemia of heart tissue. Examples are the myocardian, skeletchal or smooth muscle, artery or vein, lung, brain, kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and extremities. A particular example is after myocardial infarction or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a PR-39 protein. The specification describes PR-39 derived peptides, which are used for selective inhibition of IkappaBalpha degradation within a targeted cell collection in-situ. The method is useful for selectively inhibiting IkappaBalpha protein degradation in situ, decreasing the activity of NFkappaB transcription factor and selective control of NFkappaB-dependent gene expression in situ. The PR-39 derived peptides are useful in the treatment of myocardial infarction, chronic myocardial ischemia of heart disease and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39;
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0; Mismatches
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hes 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 AA;
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Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs
                                                                                                                                Leukocyte superoxide anion; leukocyte O2- production;
leukocyte attraction; proline-arginine-rich antimicrobial peptide;
PR-rich antimicrobial peptide; neutrophil; wound site; infection;
tissue damage; oxygen radical; antibacterial.
                                                                                                      Proline-arginine (PR)-rich antimicrobial peptide PR-39.
        ADE86112 standard, peptide; 39
                                                                                                                                                                                                                                                                                                                       07-DEC-2001; 2001US-00014147.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          (BLEC/) BLECHA F.
                                                                                                                                                                                                                                                         US2003125249-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                        10-APR-1995;
08-OCT-1997;
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                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraocular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work synergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysplasia, iridial melanocyte hyperplasia, and hyperpigmentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                        antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opnthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial peptide.
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                             ; DB 4;
2.7e-15;
                                                                                          1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP
                                                                                                                  RRRPRPYLPRPRPPFFPRLPPRIPPGFPPRFP
                                              Pred. No. 2.7
0; Mismatches
                             100.0%; Score 238; 100.0%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                              Antimicrobial peptide PR-39.
                                                                                                                                                                                                                                                                              (first entry)
                                                              39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CAYM-) CAYMAN CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-011506/01
                                                Similarity
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Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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Best Local (
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                                                     The present invention relates to a method of inhibiting leukocyte superoxide anion (02-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (FR)-ird antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, a neutrophil, to a location, e.g. a wound site. The PR-rich peptides useful as medicaments to fight infection by attracting leukocytes to known site, while restricting tissue damage at the wound site cused the secessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
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100.0%; Pred. No. 2.7e-15;
iive 0; Mismatches 0;
Claim 2; SEQ ID NO 1; 24pp; English
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1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP 39
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to inhibiting leucocyte superoxide anion (02-)
production using a naturally occurring proline-arginine (PR)-rich
artimicrobial peptide known as PR-39 and its truncated analogs. The
method comprises contacting leucocytes with the peptide comprising 39 or
26 amino acids, for a time and under conditions effective to inhibit
10 closely superoxide anion production. The peptide inhibits the activity
of NADPH oxidase responsible for anion production, by binding to Src
homology 3 (5H3) domain of p47phox, which is a 47 kDa cytosolic protein
of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or
porcine leucocyte and the mammalian leucocyte is neutrophil. Another
method is also disclosed which employs a PR-39 analog that comprise 16
amino acids, where the sum of the proline and arginine residues in the
effective peptide is at least 66 or 74 % of the total number of amino
acids. This peptide inhibits leucocyte 02- production by the effective
binding to p47phox in whole calls, therefore interfering with the binding
of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
the peptide are arginine residues. The method of the invention is useful
cor inhibiting leucocyte oxygen radical production. The peptides are
useful as medicaments for fighting infections by attracting leucocytes to
a wound site, yet restrict tissue damage at the wound site caused by
excessive and the service by these leucocytes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
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                                                                                                                                                                                                                       'note= "Essential for antibacterial activity"
                                                                                                                                                                                                                                                                                                                                  "Essential for antibacterial activity"
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 infection; wound ; tissue damage ; PR-39 peptide.
                                                                                                                                                                                                                                          11. .26
/label= PR-16_peptide
20. .26
/note= "Re---
                                                                                              l. .26
/label= PR-26_peptide
                                                                                                                                . .19
label= PR-19_peptide
                                                                                                                                                                     . .14
label= PR-14_peptide
                                                                                                                                                                                                                                                                                                                                                  25. .39
/label= PR-15_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1; 24pp; English.
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2003; 2003US-00651147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00419066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is PR-39 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-225728/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLECHA F.
SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                           US2004043934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1995;
08-OCT-1997;
                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blecha F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BLEC/) 1
(SHIJ/) 8
                                                                                          Peptide
                                                                                                                              Peptide
                                                                                                                                                                   Peptide
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The invention relates to a vaccine comprising at least one antigen and at least one cathelicidin derived antimicrobial peptide or its derivative. The vaccine is useful for active immunization, especially of humans or animals without protection against the specific antigen. The cathelicidin derived antimicrobial peptide is useful in the preparation of an adjuvant for enhancing the immune response to at least one antigen, where the adjuvant enhances the uptake of at least one antigen, where the Sequences ABB07708-15 represent C-terminal fragments of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine for active immunization or for preparing an adjuvant for enhancing an immune response to at least one antigen, comprises at least one antigen and at least one cathelicidin derived antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine, cathelicidin, antimicrobial; immunostimulant; immune response; antigen presenting cell; adjuvant; porcine; PR-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RRRPRPPYLPRPRPPPFFPPRLPPRIPPGFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 100.0%; Score 238; DB 5; Local Similarity 100.0%; Pred. No. 2.9e-15; hes 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RRRPRPPYLPRPPPFFPPRLPPRIPPGFPPRFPPRFP
                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide PR-39 C-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buschle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptides of the cathelicicidin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zauner W,
                                                                                                                                                                                       ABB07714 standard; peptide; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR82250 standard; protein; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2000; 2000AT-00001416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2001; 2001WO-EP009529
                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fritz J, Mattner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-269154/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200213857-A2.
                                                                                                                                                                                                                                                                                                                      10-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2002
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to increase the uptake of iRNA's.

Sequence 42 AA;

SXS

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08-AUG-2003;
             11-AUG-2003;
    bactenecin.
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RNA interference; iRNA; antiennse technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; oclon cancer; lung cancer; neurological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; cell permeation peptide;
cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
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Unidentified

WO2004080406-A2.

23-SEP-2004.

08-MAR-2004; 2004WO-US007070

2003US-0454265P. 2003US-0454962P. 2003US-0455050P 12-MAR-2003; 13-MAR-2003; 13-MAR-2003;

2003US-0465802P. 2003US-0469612P. 2003US-0493986P. 2003US-0462894P 2003US-0463772P 2003US-046565FP 25-APR-2003; 09-MAY-2003; 14-APR-2003; 17-APR-2003; 25-APR-2003;

2003US-0494597P. 2003US-0510246P 26-SEP-2003; 09-OCT-2003; 10-OCT-2003;

07-NOV-2003;

2003US-0510318P. 2003US-0518453P.

(ALNY-) ALNYLAM PHARM.

Manoharan M, Bumcrot D;

WPI; 2004-677362/66.

Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.

Disclosure; SEQ ID NO 6749; 378pp; English

The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have cone or more asymmetrical 2'-0 alkyl modifications, the antisense sequence targets a human gene sequence. Also described and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (M) app8-100 criticals or glucose-6-phosphatase levels in a subject; producing (I); ctabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where introducing one or more asymmetrical modification in the sequence, where critican decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (C) the subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apol-100, elevated or otherwise unwanted characterised by elevated or otherwise unwanted expression of apol-100, elevated or otherwise unwanted disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant confidence of disorder e.g. diabetes or type-2 diabetes (CAD), coronary heart chisase (CHD) and atherosclerosis (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism. C related disorder e.g. diabetes or type-2 diabetes (CAD), relating the diseases as mentioned above, cancer (e.g. breast, colon or creating the diseases as mentioned above, cancer (e.g. breast, colon or colump cancer), neurological disease (e.g., Huntington disease

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ö
                                                                                                                                Escherichia coli; B. coli; AMP gene; anti-microbial peptide; screening; preservation; food; feed; paint formulation; detergent; cosmetic; medical device; prosthetic implant; disinfectant; microbial infection;
             Gaps
             ö
Length 42;
             Indels
                           39
                                         39
                                  1 RRRPRPDYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP
                           1 RRRPRPPYLPRPPPFFPPRLPPRIPPGFPPRFPPRFP
100.0%; Score 238; DB 8;
100.0%; Pred. No. 2.9e-15;
ive 0; Mismatches 0;
                                                                                                                    E. coli AMP gene PR39 amino acid sequence.
                                                                            AAB51194 standard; peptide; 44 AA
                                                                                                       22-MAR-2001 (first entry)
              39; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                     Escherichia coli.
                                                                                           AAB51194;
               Matches
                                                               RESULT 14
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29-MAY-2000; 2000WO-DK000287. 99DK-00000766 (NOVO ) NOVO NORDISK AS WPI; 2001-070965/08. Kristensen H; 31-MAY-1999;

WO200073433-A1.

07-DEC-2000.

Screening for nucleotide sequences encoding antimicrobial peptides by generating peptide libraries in microorganisms, inducing expression of peptides, selecting cells and recovering nucleotide sequences from cells.

Example 1; Page 34; 59pp; English

The present invention describes a plasmid which is ligated with a pool of nucleotide sequences (NT) linked to an inducible promoter, to express a peptide (P) (an enzyme or mature (P) of less than 100 amino acids of peptide (P) (an enzyme or mature (P) of less than 100 amino acids of coptionally linked to a signal (P)), transformed into host cells and cultured in presence of an inducer to induce expression of the NT. A method of screening (I) a pool of nucleotide sequences to select a meleotide sequence encoding a peptide, comprises: (a) ligating a plasmid with the pool of NT; (b) transforming host cells which are sensitive to the peptide with the ligated plasmids; (c) screening the transformed cells to select viable cells; (d) cultivating the viable cells in the presence of an inducer to induce expression of NT; (e) selecting cells according to the effect of the inducer on cell growth; and (f) recovering according to the effect of the inducer on cell growth; and (f) recovering correcting a pool of nucleotide sequences to select a nucleotide sequence cencoding a peptide which is an antimicrobial peptide or an antimicrobial cenzyme active on bacteria and for finding and preparing a composition for treatment of human or animal. The antimicrobial peptide obtained using continual or animal. (I) may be employed in preservation of e.g. food/feed, paint formulations, detergents, cosmetics, medical devices such as prosthetic implants and also to disinfect and/or kill microbial cells on an object e.g. as an disinfectant for the treatment of biofillm. The peptides are useful for treating microbial infections and/or tumours. Peptides with improved bio-activity can be developed using (I). The peptides have no ω

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AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first cantimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first cantimicated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. These sequences, and PR39, can be used in the method of the invention. The method comprises administering to a leukocyte a coptide (such as this sequence) capable of inhibiting leukocyte of production. The peptides can be used as medicaments for fighting tissue infection by attracting leukocytes to a wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; bank synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
negative effect on normal mammalian and/or eukaryotic cells. The present sequence represents an AMP (antimicrobial peptide) gene amino acid sequence, which is used in an example from the present invention
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39
                                                                                                                                                 ;
0
                                                                                                           Length 44;
                                                                                                                                               0; Indels
                                                                                                                                                                                    39
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                                                                                                                                                                                    1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP
                                                                                                                                                                                                         RRRPROPYLPROPEFFPRILPBRIPGFFPRFF
                                                                                                           100.0%; Score 238; DB 4;
100.0%; Pred. No. 3e-15;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Leukocyte O2- production inhibitor peptide PR26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                AAW01447 standard; peptide; 26 AA.
                                                                                                             100.0%; Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 26; 45pp; English.
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                                                                                                                                                 Conservative
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                                                                                                     Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
                                                                          Sequence 44 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blecha F,
                                                                                                                                                                                                                                                                                                                                                     AAW01447;
                                                                                                                                                                                                                                                                              RESULT 15
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Length 26;

65.1%; Score 155; DB 2; I 100.0%; Pred. No. 8.7e-08;

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Gaps
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Indels
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0
0; Mismatches
                  56
                1 RERPEPYLPRPRPPFFPPRLPPRI
                                   1 KREPRPPYLPRPRPPFFPPRLPPRI
26; Conservative
Matches
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                                  요
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Search completed: October 26, 2005, 05:12:03 Job time : 158.518 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein Run on:

October 26, 2005, 05:00:14 ; Search time 29.0727 Seconds (without alignments) 129.071 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-014-147-1 238 1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRPP 39

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	antimicrobial prot	extensin class I (	cathelin-like anti	hybrid proline-ric	hypothetical prote	PE			hypothetical prote	chitinase (EC 3.2.	extensin homolog -	rgi	ហ	bactenecin 7 - bov	proline-rich prote	unknown protein F1	hypothetical prote	immediate-early pr	proliferation pote	proline-rich prote	spliceosome-associ	spliceosome-associ	Wiskott-Aldrich sy	wiskott-aldrich sy	retinoblastoma bin			Ų,	hypothetical prote
ΠD	568232	ß				S40463				851939	T07176					_				JC5572				T38819	. AS7640	T10064		110	B40505
h DB	2 2					8																80	4	4	8	6	-	6	8
Length	17.	19	212	30	997	22	42	1006	134	43	221	38	176	S	148	54	494	146			42	38	57	57	94	32	14	59	195
% Query Match	100.0	51.5	46.0	15.0	14.3	13.1	11.4	11.2	11.0	99.6	39.7	39.7	39.5	39.1	38.9	38.9	38.7	38.7	38.4	38.2	38.2	38.0	38.0	38.0	38.0	37.8	37.4	37.4	37.2
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Score	238	122.5	109.5	107	105.5	102.5	98.5	98	97.5	95	94.5	4.	94	93	92.5	92.5		92	91.5	6	93	90.5	ö	90.5	ö	8	89	8	88.5
Result No.		7	٣	4	J.	φ	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

sulfated surface g probable transcrip cysteine-rich exte	cell wall protein nuclear protein EB formin isoform IV	formin - mouse C-terminal domain-	Ballyaly process proline proline proline proline.	circumsporozoite p acrosin (EC 3.4.21	acrosin (EC 3.4.21 OmpA family protei hydroxyproline-ric
A33647 T08599 B48232	S52985 S42442 S24407	S11515 T31420	S10782 PJHUSB S09779	OZZQMY A34170	S47538 D87682 S06733
000	000	000	7 7 7		0 0 0
485 1098 196	381 487 1206	1468	57 79 322	367 415	431 449 620
37.0 36.8 36.6	36.6	36.6	36.1 36.1 36.1	36.1 36.1	36.1 36.1 36.1
88 87.5 87	87 87 87	86.5	98 98 88 88	86 86	9 8 8 8 8 8
30 31	ነ ርዕ ርዕ ነ ርዕ ርዕ ነ ርዕ ረቅ ርዕ	36	8 8 8 8 9 0	41	4 4 4 4 4 5 5

#### ALIGNMENTS

	RESULT 1
	1000000
	antimicrobial protein Pk-39 preduction; Cathelin-associated Prig
	NATICELIACIE Indicate MICE Admedition (domedition described)
-	C.peciles as peril composition 13-Mar-1997 #text_change 09-Jul-2004
	C. Accession: S68232; JN0899; <u>1</u> 47138; S19563
•	R; Zhao, C.; Ganz, T.; Lehrer, R.I.
	FEBS Lett. 376, 130-134, 1995
	A, Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni
	A;Reference number: S68232; MUID:96105365; PMID:/498526
	A; Accession: Selection and the control of the cont
	ASSTATUS TRANSPACTOR NO. SHOWN
	Afrolecule Lype: DAA N.Doedidies 1.172 / 77Hb.
_	A.Cross-references: UNIPROT: P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g1165
	A. Experimental source: leukocytes
	R;Storici, P.; Zanetti, M.
_	Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
	A,Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the
	A Reference number: UNUBY9; MULD:940/1853; FMID:8250003
	A; Accession: unusay
	A; Molecule Cype: mixwa
	A; KESIQUES: 1-20; A; 22-114 < 510.
	ACTORS-relevences designately assets and actors are second as a new control of the control of th
	Ajaxperimental Boulete: Doue marion, wearing to Ajaxperimental Bouleteson, K.; Andersson, L.; Bome Bouleteson, C. H. Machineson, K. P.; Chowdharv, B.P.; Johansson, M.; Andersson, L.; Bome
	Nyduallulusepout, 611.5; 192.7089, 1995
-	A.T.: Mari Mari Tructure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami
	A: Reference number: I47138; MUID:95350216; PMID:7624374
	A;Accession: 147138
	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
	A;Residues: 1-28,'T',30-89,'QR',92-116,'NDP',120-172 <gud></gud>
	A; Cross-references: EMBL: X87236; NID: g829142; FIDN: CAACOES; FID: SID: SID: SID: A. Toernvall
	R; Agerberth, B.; Lee, J.Y.; Bergman, T.; Cariguist, M.; Boman, n.G.; Mucc, V.; Coccinert,
	Bur. U. Blochem. 202, 849-849, 1991 Bur. U. Blochem. 202, 849-849, 1991 Bur. U. Blochem. 202, 849-849, 1991
	A)TILLE: AMINO ACID BEQUENCE OF EX-3: ISOTALION INCOLLENCE OF EX-2: ISOTALION AND AND AND AND AND AND AND AND AND AN
	A; Arression: S19563
	A:Molecule type: Drottein
	A: Residues: 131-169 < AGE>
	A: Experimental source: intestine
	CiGentics:
	A;Gene: PR39
	A; Introns: 66/3; 102/3; 126/3
	C; Superfamily: cathelin; cystatin homology
	C; Keywords: amidated carboxyl end; antibacterial
	F;1-29/Domain: signal sequence #status predicted <sig></sig>
	F;22-129/Domain: cystatin homology <crs></crs>
	F;30-130/Domain: properties #status pressures exercises experimental <a href="Mailto:MAT">MAT</a>
_	F/131-169/Product: ancimicrobial process execute experimental

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site: amidated carboxyl end (Pro) (amide in mature form from following

F;169/Modified

Matches

RESULT 2

```
prophenin (PP-2) precursor - pig
NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor '
NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor '
C;Species: 03.8 serofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: $40463; $573131; $68333
FBBS Lett. 336, 284-288, 1993
A;Pitle: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial I
A;Reference number: $40463; MUID:94085623; PMID:8262247
                                                                                                                                                                                                              A;Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein. A;Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein. A;Reference number: J01663; MUID:92361259; PMID:1498600
A;Accession: J01663
A;Accession: J0163
A;Residues: 1.301 <J08>
A;Residues: 1.301 <J08>
A;Residues: UNIPROT:Q41848; EMBL:X60432; NID:g433706; PIDN:CAA42959.1; PID:g43370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1.597 <MIL>
A;Residues: 1.997 <MIL>
A;Cross-references: UNIPROT:Q9GYL4; EMBL:U41538; PIDN:AAC48181.1; GSPDB:GN00028; CESP:R04
A;Experimental source: strain Bristol N2; clone R04E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caemorhabditis elegans
C;Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                           C;Speciës: Zea mays (maize)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 PTPPYVPPTPRPSPPPYVPPTPRPSPPYVPPTPP 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PRPPYL---PRPRPPFFPPRLPPR---IPPGFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 216/3; 234/3; 255/2; 305/1; 669/3; 891/1; 986/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riviller, N. submitted to the EMBL Data Library, December 1995 submitted to the EMBL Data Library, December 1995 A;Description: The sequence of C. elegans cosmid R04E5. A;Reference number: Z20535 A;Reference number: Z20535 A;Accession: T28972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.3%; Score 105.5; DB 2;
55.8%; Pred. No. 0.026;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein R04E5.8 - Caenorhabditis elegans
                                                                                                                                                                                    R, Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.0%; Score 107; DB 2; 50.0%; Pred. No. 0.0064;
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A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain W64A C; Superfamily: hydroxyproline-rich glycoprotein
                                                                 hybrid proline-rich protein - maize
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Best Local Similarity 50.09
Matches 21, Conservative
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Best Local Similarity 55.89
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A;Molecule type: mRNA
A;Residues: 1-228 <PUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:R04E5.8
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                                                                                                                                                         C; Accession: JQ1663
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: 1-212 (STR>
A;Cross-references: UNIPROT: P51524; GB:X86031; NID:g1006756; PIDN:CAA60023.1; PID:g10067
R;Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I
FEBS Lett. 362, 65-69; 1995
A;Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine 1
A;Reference number: S68726; MUID:95212585; PMID:7698355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S57330
Cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)
NyAlternate names: antimicrobial peptide; prophenin-1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57330; S68726
R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V Biol. Chem. Hoppe-Seyler 376, S07-S10, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A;Reference number: S57330; MUID:96042752; PMID:7576250
                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S14981
R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response A;Reference number: S14970; MUID:91329690; PMID:1714316
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                                                                                                                                                                                                                                                                                                                                             extensin class I (clone w1-8 L) - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
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      Length 172;
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Pred. No. 0.00019;
3; Mismatches 10; Indels
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                                                                 0; Indels
                                                                                                                                                             69 REPREPEREPERTLEPEREPEREGYLEPERKYPF 106
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ch 100.0%; Score 238; DB 2; 1 Similarity 100.0%; Pred. No. 1.2e-14; 39; Conservative 0; Mismatches 0;
                                                                                                                               1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: cv. UC82B
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: cell wall; glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Experimental source: leukocytes
C.Superfamily: cafhelin; cystatin homology
C.Supords: antibacterial
F.6-113/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.9%;
Matches 22; Conservative
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Matches 29; Conserv
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A,Molecule type: mRNA
A,Residues: 1-199 <SHO>
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      Query Match
Best Local (
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RESULT 3

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A; Molecule type: mRNA
A; Residues: 191-397 <BER2>
C; Genetics:
                                                                                                          A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1006 <STO>
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                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Readiues: 1-228 <STR>
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
A;EBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen
A;Reference number: S68232; MUID:96105365; PMID:7498526
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 1-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 08-Dec-1995
C;Accession: B36589
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
T;Biol. Chem. 265, 18871-18874, 1990
A;Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides (A;Reference number: A36589; MUID:91035404; PMID:2229048
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| Molecule type: DMA
| Residues: 1-228 <2HA>
| Residues: EMBL:X89202; NID:G1165148; PIDN:CAA61488.1; PID:G1165149
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 43.1%; Score 102.5; DB 2; Length 228; Local Similarity 51.9%; Pred. No. 0.012; nes 28; Conservative 1; Mismatches 6; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 41.4%; Score 98.5; DB 2; Length 42; I Similarity 52.4%; Pred. No. 0.006; 22; Conservative 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-228/Product: prophenin (PF-2) #status predicted <MAT>
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A;Molecule type: protein
A;Residues: 1-42 <FRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B36589
                                                                                                                                                                                                                                                                                                                                                      A; Accession: S68233
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Richard S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. R;Lin, X.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-134 <STO>
A;Cross-references: UNIPROT:Q9XIP3; GB:AE002093; NID:g5306259; PIDN:AAD41991.1; GSPDB:GN(
                                                                                                                                                                                                                                                                                A;Cross.references: UNIPROT:Q9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A;Residues: 1-439 <BER>
A;Cross-references: UNIPROT:Q42421; EMBL:X79301; NID:g488730; PID:g488731
A;Note: the authors translated the codon TGC for residue 416 as Gly
A;Accession: S72315
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1006;
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53.8%; Pred. No. 0.021;
tive 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 248/1; 300/2
C;Keywords: glycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-439/Product: chitinase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PRPPYLPR-PRPPFFPPRLPPRIPPGF--PPRFPPRFP
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Best Local Similarity 53.8<sup>†</sup>
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.8<sup>†</sup>
Matches 20, Conservative
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proline-rich protein V-beta 1 precursor - rat
C;Species: Rattus norregicus (Norway rat)
C;Daccies: G-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A51118; S39206
R;Courty, Y.; Rosinski-Chupin, I.; Rougeon, F.
J. Blol. Chem. 269, 520-527, 1994
A;Fitle: A new proline-rich protein precursor expressed in the salivary glands of the rat
A;Reference number: A53118; MUID:94103265; PMID:8276845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Superfamily: cathelin, cystatin homology
C;Superfamily: cathelin, cystatin homology
C;Reywords: amidated catboxyl end; antibacterial
F;1.29/Domain: signal sequence #status predicted <SIG>
F;20-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;31-13/Product: neutrophil antibiotic protein Bac5 #status predicted <MAT>
F;131-173/Product: amidated carboxyl end (Pro) (amide in mature form following gl)
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A;Note: submitted to the EMBL Data Library, July 1993
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Cispecies: Bos primigenius taurus (cattle)
Cispecies: L2-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997
Ciscossion: A36589
Right R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
Rightank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
A; Frank, Chem. 265, 18871-18874, 1990
A; Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of A; Reference number: A36589; MUID:91035404; PMID:2229048
                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-176 <ZAN>
A;Cross-references: UNIPROT:P19660; GB:L02650; NID:g162730; PIDN:AAA30404.1; PID:g162731
A;Note: sequence extracted from NCBI backbone (NCBIP:121443)
                                                                                                                                                              C,Accession: A45328
R;Zanetti, M.; Del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.
Biol. Chem. 268, 522-526, 1993
A;Title: The CDNA of the neutrophil antibiotic Bac5 predicts a pro-sequence homologous A;Reference number: A45328; MUID:93107055; PMID:8416958
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                            bactenecin 5 precursor - bovine
NiAlternate names: Bac5, neutrophil antibiotic protein 5
C:Species: Bos primigenius taurus (cattle)
C:Species: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.5%; Score 94; DB 2; Best Local Similarity 54.1%; Pred. No. 0.055; Matches 20; Conservative 1; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.1%; Score 93; DB 2;
Best Local Similarity 61.5%; Pred. No. 0.025;
Matches 24; Conservative 0; Mismatches 13
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A,Molecule type: protein
A,Residues: 1-59 <FRA>
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A; Residues: 1-148 <COU>
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      extensin homolog - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Species: Solanum tuberosum (potato)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C;Accession: T07176

R;Macleod, M.R.

Bimacleod, M.R.

A;Reference number: Z15977

A;Reference number: Z15977

A;Accession: T07176

A;Accession: T07176

A;Accession: T07176

A;Accession: T07176

A;Coserred pre: mRNA

A;Residues: 1-221 < MAC>

A;Coserreferences: UNIPROT: 049946; EMBL: AJ003220; NID:e1251331; PIDN: CAA06000.1; PID:e1

C;Superimental source: cv. Record; swelling stolon

C;Superfamily: glutelin
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R;Bengtsson, E.; Neame, P.J.; Heinegard, D.; Sommarin, Y.
Biol. Chem. 270, 25639-25644, 1995
A;Title: The primary structure of a basic leucine-rich repeat protein, PRELP, found in A;Reference number: I39068; MUID:96029653; PMID:7592739
A;Accession: I39068
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-382 <RES>
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A;Map position: 1432.1
C;Superfamily: fibrondulin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 RRPRPGTGPGRRPRPRPTPSFPQPDEPAEPTDLPPPLPPGPPSIFPDCPRECYCPDF 83
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C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
                                                                                                                                         Gaps
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                                                         ch 39.9%; Score 95; DB 2; Length 439; I Similarity 55.3%; Pred. No. 0.1; 21; Conservative 0; Mismatches 15; Indels
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F;183-423/Domain: plant chitinase homology <PCH>
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Matches 21; Conserv
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Query Match

RESULT 11

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Best Loca Matches

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RESULT 12

Query Match Best Local Matches 2

RESULT 13

8

Genetics:

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9; Gaps
C,Genetics:
A,Gene: VCS-beta1
A,Introns: 18/3
C,Superfamily: proline-rich peptide P-B
C,Keywords: glycoprotein
F,1-18/Domain: signal sequence #status predicted <SIG>F;19-148/Product: proline-rich protein V-beta 1 #status predicted <WAT>F;133,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                            Query Match 38.9%; Score 92.5; DB 2; Length 148; Best Local Similarity 52.3%; Pred. No. 0.063; Matches 23; Conservative 0; Mismatches 12; Indels 5
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3

Search completed: October 26, 2005, 05:19:57 Job time : 31.0727 secs

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147.844 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                 1612378 segs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Result No.

Q6sse8 chlamydomon	Q9dvw0 plutella xy	_	O35328 mus musculu	Q9r0i7 mus musculu	Q9gkn8 bos taurus	Q69858 oryza sativ	Q96jh1 homo sapien	Q6zd62 oryza sativ	Q42421 beta vulgar	Q86ya8 homo sapien	Q8nbb9 homo sapien	Q8nf45 homo sapien	Q7q8p5 anopheles g	
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97.5	97	97	96	96	95.5	95.5	95.5	95	95	95	95	95	94.5	
3.2	33	34	35	36	37	38	39	40	41	42	43	4	45	

### ALIGNMENTS

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TISSUE=Neutrophils;
MEDINDE=95088504; PubMed=7996056;
Shi J., Ross C.R., Chengappa M.M., Blecha F.;
"Identification of a proline-arginine-rich antibacterial peptide from
                                                                                                                                                                                                                              MEDILINE=95550216; PubMed=7624374; MEDILINE=95550216; PubMed=7624374; Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M., Andersson L., Boman H.G.; Extructure of the gene for porcine peptide antibiotic PR-39, a cathelin gene family member: comparative mapping of the locus for the human peptide antibiotic FALL-39."; Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Amino acid sequence of PR-39. Isolation from pig intestine of a new member of the family of proline-arginine-rich antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3; Zhao C., Ganz T., Lehrer R.I.; "Structures of genes for two cathelin-associated antimicrobial peppides: prophenin-2 and PR-39.";
                                                                                                                                Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bone marrow;
MEDLINE=94071853; PubMed=8250863;
Storici P., Zanetti M.;
"A cDNA derived from pig bone marrow cells predicts a sequence identical to the intestinal antibacterial poptide PR-39.";
Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB=Intestine;
MEDLINE=92111534; PubMed=1765098;
Agerberth B., Lee J. Y., Bergman T., Carlquist M., Boman H.G.,
Mutt V., Joernvall H.;
                                   01-MAR-1992 (Rel. 21, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Antibacterial protein PR-39 precursor.
            172 AA
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            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EBS Lett. 376:130-134(1995)
            STANDARD;
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                            09TR84;
          PR39 PIG
P80054; Q9TR8
01-MAR-1992 (1
01-OCT-1996 (1
05-JUL-2004 (1
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                                                                                                                  Name=PR39;
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PR39_PIG
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SEQUENCE FROM N.A. STRAIN=17XNL;
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Q9XIZ3;
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                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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neutrophils that is analogous to PR-39, an antibacterial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                   the small intestine.";
J. Leukoc. Biol. 56:807-811(1994).
-!- FUNCTION: Exerts a potent antimicrobial activity against both
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081LQ0;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Spliceosome-associated protein, putative.
0RFNames-FF14 0194;
Plasmodium falciparum (isolate 3D7).
Elasmodium falciparum (solate 3D7).
Elasmodium falciparum (solate 3D7).
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Pyrrolidone carboxylic acid (By
                                                                                                                                                                         E.coli and B.megaterium.
1- TISSUE SPECIFICITY: Small intestine and bone marrow.
1- SIMILARITY: Belongs to the cathelicidin family.
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994B792798C0E133 CRC64;
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G -> A (in Ref. 2).

A -> T (in Ref. 1).

RQ -> QR (in Ref. 1).

IHS -> NDP (in Ref. 1).

P -> I (in Ref. 5).
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EMBL; L23825; AAA1109.1; -.
EMBL; X89201; CAA64487.1; -.
PIR; S68232; S68322.
HSSP; P32196; IKWI.
InterPro; IPR001894; Cathelicidin.
Probom; P000666; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Anidation; Antibiotic; Direct protein sequencing; PATOLidone carboxylic acid; Signal.
Signal
Signal
12 Potential.
30 Notice carboxylic cond; Signal.
RADD_RES 30 Notice carboxylic in Principle Catherial protein Properties Catherial Properties Catherial C
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169
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107
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DISULFID
MOD_RES
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Best Local
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Gaps
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Zea mays PMP gene. (X60432).
Oryza sativa (japonica cultivar-group).
Oryza, viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Rorsdden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                       53.6%; Score 127.5; DB 2; Length 484; 62.2%; Pred. No. 0.002; tive 0; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
49.6%; Score 118; DB 2; Length 333;
Best Local Similarity 51.2%; Pred. No. 0.009;
Matches 21; Conservative 3; Mismatches 15; Indels
                                                                                                                   "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Nagamura Y., Yamamoto K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023482; BAA78762.1; -.
HSSP; P24337; 1HYP.
                                                                                                                                                                                                      EMBL; AE014819; AAN36806.1; -.
HSSP; P11940; 1CVJ.
INTEFPTO; IPRO00564; RNA_rec_mot.
PRO0076; RRM_1; 2.
PRANT; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
SEQUENCE 484 AA; 53722 WW; 0858953D48F72E2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF00234; Tryp alpha_amyl; 1.
SMART; SM00499; AAI; 1.
SEQUENCE 333 AA; 34823 MW; 268DEC74E20E8194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 RPPFTPPYVPSPPYVPPYIPPPTVPPYVPPYIPPTPPYVP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRPRPPYLPRPRP--PPFFPPRLPPRIPPGFPPRFPPRFP 39
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Splicing factor 3b subunit 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 PPILPPNFPPTLPPNFPPTLPPNFPPGFPPNLPPNFP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PPYLP --- RPRPPPFFPPRLPPRIPPGFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 62.27
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003612; AAI
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                                                                                                                                                  falciparum.";
Nature 419:498-511(2002)
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P0482C06.8)
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REPEAT
SEQUENCE
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Q657Y0;
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REPEAT
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                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prophenin-1, an exceptionally proline-rich antimicrobial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular cloning and identification of a novel porcine cathelin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95212585; PubMed-7698355; DOI=10.1016/0014-5793(95)00210-Z; Harvig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C., Lehrer R.I.;
                                                                                                                                          "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nautre 419:512-519 (2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                              Gaps
        Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabbi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Salzberg S.L., Venter J.C., Waters A.P., Salth H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    porcine leukocytes.";

FEBS Lett. 362:65-69(1995).

-!- FUNCTION: Exerts antimicrobial activity. It is more effective against cram-negative bacteria than Gram-positive bacteria.

-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                     DB 2; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strukelj B., Pungercar J., Kopitar G., Renko M., Lenarcic B.,
Berbic S., Turk V.,
                                                                                                                                                                                                                                                                                           415 AA; 46441 MW; 6D9D28AF80357B0A CRC64;
                                                                                                                                                                                                                                                                                                       46.4%; Score 110.5; DB 2; FS 9%; Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                         291 PPNLP-PNLPPNLPPNLPPNLPPNLP 323
                                                                                                                                                                                                                                                                                                                                                                          6 PPYLPRPRPPFFPPRLPPRIPPGFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Prophenin-1 precursor (PF-1) (C6) (Fragment).
                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial peptide precursor.";
Biol. Chem. Hoppe-Seyler 376:507-510(1995)
  PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                preliminary data.
EMBL; AABL01000316; EAA20492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Bone marrow;
MEDLINE=96042752; PubMed=7576250;
                                                                                                                                                                                                                                        HSSP; P11940; 1CVJ.
InterPro; IPR000504; RNA_rec_mot.
InterPro; IPR00050, RNM_1; 2.
PROSITE; PSS0102; RRM; 2.
SEQUENCE 415 AA; 46441 MW; 6D
                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF11 PIG
P51524;
                                                                                                                                                                                                                                                                                                                        Query Match
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Dubmed=12447438;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Sasaki T., Matsumoto T., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Maeukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Itch T., Itoh T., Itoh Y., Itoh Y., Kobayashi N., Komo I., Karasawa W., Kategiri S., Kikuta A., Kobayashi T., Mukai Y., Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y., Nakashima M., Nakamima M., Nakamima M., Nakamima M., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRPR-----PRYLPRPR-PPFFFP-PRLPPRIPPGFP-PRFP-----PRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By similarity.
Proline amide (G-210 provides amide
                                                                                                                                                                                                                                                                                                                                                            Removed in mature form (Potential). Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109.5; DB 1; Length 212;
Pred. No. 0.031;
1; Mismatches 5; Indels 19.
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein P0005A05.30 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A315414C90DBF423 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro-rich.
7 X 10 AA tandem repeats.
                                    EMBL, X86011; CAA60023.1; -.
PIR; S57310; S57330.
HISSP, P32196; 1LXE.
InterPro; IPRO101894; Cathelicidin.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Amidation; Antibiotic; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
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                                                                                                                                                                                                  Pyrrolidone carboxylic acid; Repeat; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                Prophenin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
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                                                                                                                                                                                                                                                                                                                        Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
or send an email to license@isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23956 MW;
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Best Local Similarity 53.77
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                     130
209
212
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151
161
171
181
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1132
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NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=HRGP gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=HK10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                             Q9SBM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GYL4
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                                                                                                                                                                                                                              Gaps
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MEDLINE=92361259; PubMed=1498600;
Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
"A maize embryo-specific gene encodes a proline-rich and hydrophobic
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Titanji V.P.K., Souopgui J., Goghomu S.M., Nde P.N., Lucius R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF055985, AAC12760.1; -.
SEQUENCE 93 AA, 9785 WW; 80C2F2EB0DE27D17 CRC64;
                                                                                                                                                                                                                           13;
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                                                                                                                                                                                                                                                                                           45.6%; Score 108.5; DB 2; Length 236; 51.0%; Pred. No. 0.041; Live 1; Mismatches 10; Indels 13.
                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                    2 RRPRPPY-----LPRPRPPPFFPPRLPPRI-----PPGFPPRFPPR
                   Yano M., Jiang J., Gojobori T.;
"The genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107.5; DB 2; Length Pred. No. 0.021; o; Mismatches 12; Indels
                                                                              EMBL, AP002863; BAD44889.1; -.
EMBL, AP002843; BAD44850.1; -.
Hypothetical protein.
SEQUENCE 236 AA; 24666 MW; DAC94868D2903ED2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 RPPYLPRPRPPREPPRIPPRIPPGFP----RFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 RPPTTPTPTPPPPPRGFPRIPPPPPIQGRASFPPPPP 60
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Last sequence update)
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01-AUG-1998 (TrEMBLrel. 07, C1
01-AUG-1998 (TrEMBLrel. 07, La
01-MAR-2004 (TrEMBLrel. 26, La
Pyrrolidone-rich antigen.
Name=Ov42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cn 45.2%;
1 Similarity 57.5%;
23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q41848;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NAR-2004 (TrEMBLrel. 26,
Prolin rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flant Cell 4:413-423(1992)
EMBL, X60432, CAA42959.1;
PIR, JQ1663, JQ1663.
HSSP, P24337; 1HYP.
                                                                                                                                                                               Query Match
Best Local Similarity 51.09
Matches 25; Conservative
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InterPro; IPR003612; AAI.
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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O61649
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Q41848
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; CD0749C6AF02BD74 CRC64;
                                                                                                                                                    Gaps
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"Response to the sexual pheromone and wounding in the green alga volvox: induction of an extracellular glycoprotein consisting almost exclusively of hydroxyproline.";
J. Biol. Chem. 274:35023-35028 [1999).

GO: GO:0005199; F:structural constituent of cell wall; IEA.
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales, Volvox.
Volvocaceae, Volvox.
NCBI_TaxID=3068;
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                                                                                            45.0%; Score 107; DB 2; Length 301;
llarity 50.0%; Pred. No. 0.07;
Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                            169 PTPPYVPPTPRPSPPPYVPPTPRPSPPYVPPTPP 210
Pfam; PF00234; Tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;
                                                                                                                                                                                                4 PRPPYL---PRPRPPFFPPRLPPR---IPPGFPPRFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                           QSSBM1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hydroxyproline-rich glycoprotein DZ-HRGP precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein R04E5.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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60.6%; Pred. No. 0.11;
iive 0; Mismatches 13
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MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 60.69
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                     Query Match
Best Local Similarity
The 21; Conserve
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Conservative
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217
157
167
177
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 19;
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PEPTIDE
PROPEP
MOD_RES
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  Matches
                                                                                             RESULT 12
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wing R.A., Yu Y', Soderlund C., Kim H.-R., Rambo T., Currie J., Collura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.3%; Score 103; DB 2; Length 351; 57.6%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                             Score 105.5; DB 2; Length
Pred. No. 0.29;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Wormbas Mosttium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                         WormPep; R04E5.8a; Levacour.

Hypothetical protein.

ProvienCE 997 AA; 111954 MW; F1620378EF0D9DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RRPR--PPYLPRPRPPPPP---RLPPRIPPGFPPRFPPRFP 39
                                                                    "The sequence of C. elegans cosmid R04E5.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                        Wilson R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein OJ1041F02.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AC135206; AAP06858.1; -...
Gramene; O84090; -...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0008270; F:nucleic acid binding; IEA.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR000690; Znf_matrin.
InterPro; IPR003604; Znf_matrin.
SMART; SM00355; ZnF_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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WormPep; R04E5.8a; CE04800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50171; ZF MATRIN; 1. Hypothetical protein. SEQUENCE 351 AA; 38984 MW;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.8%;
Matches 24; Conservative
    Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                   EMBL; U41538; AAG00010.1; -. PIR; T28872; T28872.
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                                                                                                                                                   Submitted (MAY-2003)
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Best Local Similarity
                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                       Waterston R.
                                                            Miller N.;
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Q84Q90;
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 Gaps
                                                                                                                                                                                                                                                                                                                                      PEQUENCE FROM N.A.
TISSUB-Bone marrow;
MEDLINE=94085623; PubMed=8262247; DOI=10.1016/0014-5793(93)80821-B;
MEDLINE=94085623; PubMed=8262247; DOI=10.1016/0014-5793(93)80821-B;
MEDLINE=94085623; PubMed=8262247; DOI=10.1016/0014-5793(93)80821-B;
Gubensek F., Turk V.;
"Molecular cloning of a putative homolog of proline/arginine-rich
"Molecular cloning of a putative homolog of proline/arginine-rich
antibacterial peptides from porcine bone marrow.";
FEBS Lett. 336:284-288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
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InterPro; IPR001894; Cathelicidin.
Pfam, PF00666; Cathelicidins; 1.
ProDom; PD01818; Cathelicidin; 1.
PROSITE; PS00947; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Amidation; Antibiotic; Pyrrolidone carboxylic acid; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i.- FUNCTION: Exerts antimicrobial activity. It is more effective against Gram-negative bacteria than Gram-positive bacteria.
                                                                                                                                                                                                                                            Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Removed in mature form (Potential). proline amide (G-226 provides amide group) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao C., Ganz T., Lehrer R.I.; "Structures of genes for two cathelin-associated antimicrobial peptides: prophenin-2 and PR-39."; FEBS Lett. 376:130-134(1995).
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                                                                                                                                                    PF12_PIG STANDARD; PRT; 228 AA.
P51525;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Prophenin-2 precursor (PF-2) (PR-2) (C12) (Prophenin-1 like).
 Indels
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7 X 10 AA tandem repeats.
 14;
                                                                 265 ркрррроурррродрррррридристрр 297
                                   36
 0; Mismatches
                                   4 PRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPP
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PRELIMINARY;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Moore T. Max S.I., Wang J., Hsiah F.K.,
A Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willing M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Dickson M.C.,
A Krozwinski M.I., Schalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                               39
                                                                                                                               2 RRPR-----PPYLPRPR-PPPFFP-PRLPPRIPPGFP-PRFP-----PRFP
                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                             DB 1; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.1%; Score 102.5; DB 2; Length 640; Best Local Similarity 57.9%; Pred. No. 0.34; Matches 22; Conservative 0; Mismatches 15; Indels 1;
Pyrrolidone carboxylic acid (By
                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases EMBL; BC065662; AAH65662.1; -. ZFIN; ZDB-GENE-040426-1829; zgc:77390.
            similarity).
By similarity.
By similarity.
1EA4511FF35CC182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 AA; 68823 MW; 95191F8DC32BBFF9 CRC64;
                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein zgc:77390. ORFNameszgc:77390; Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                          ch 43.1%; Score 102.5; DE Similarity 51.9%; Pred. No. 0.13; 28; Conservative 1; Mismatches
                                                                                                                                                                                                                          640 AA
                                                                                                                                                                                                                                                    (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                          PRT;
                       85 96 B
107 124 B
228 AA; 25855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
                                                                                                                                                                                                                          PRELIMINARY;
                    96
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                   05-JUL-2004
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                       DISULFID
                                                   SEQUENCE
                                                                         Query Match
Best Local
                                     DISULFID
MOD_RES
                                                                                                                                                                                                                                        Q6P0D5;
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417 RGPMPRLLP-PGPPPGRPPGPPPGLPPGPPRGP 453

RESULT 14

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUB-Brain;

STRAIN-C57BL/6; TISSUB-Brain;

STRAIN-C57BL/6; TISSUB-Brain;

STRAIN-C57BL/6; TISSUB-Brain;

STRAIN-C57BL/6; TISSUB-Brain;

STRAIN-C57BL/6; TISSUB-Brain;

Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. A., Backer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. B., Buecow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., McZewan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO51913, AAH51961.1; -.
HSSP; 079400; 1UZC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 890 AA; 101202 MW; 3513E5DCC2E4FD3E CRC64;
080W14;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
2610317D23Rik protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PRPPYLPRPPFFPPRLPPRI -- PPGFPPRFPP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1925583; 2610317D23Rik.
InterPro; IPR002713; FF.
InterPro; IPR01202; WW_Rsp5_WWP.
Pfam; PF01846; FF; 5.
Pfam; PF00397; WW; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01159; WW DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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Best Local Similarity 57.1<sup>§</sup>
Matches 20; Conservative
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SMART; SM00456; WW; 2.
                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                    Name=2610317D23Rik;
                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
STRAIN=WSS76;
STRAIN=WSS76;
SPAIN=WSS76;
SPAIN=WSS76;
STRAIN=WSS76;
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42.6%; Score 101.5; DB 2; Length 135;
Best Local Similarity 44.7%; Pred. No. 0.095;
Matches 17; Conservative 5; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
135 135
135 AA; 14829 MW; 500634A98BA49408 CRC64;
Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 37:10766-10779(1998).
EMBL; AF066072; AAC19124.1; --
DictyBase; DDB0185060; pspB.
NON_TER 13 13
NON_TER 135 AA; 14829 MW; 5006
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1;

3; Gaps

S RPPYLPRPRP---PPFFPPRLPPRIPPGFPPRFP 39 21 QPPTYPPTQPPTYPPSYPPSYPPSYPPTHPPTYP 58

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Search completed: October 26, 2005, 05:18:30 Job time : 140.082 secs

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                                                                                 October 26, 2005, 05:02:04; Search time 40.0636 Seconds (without alignments) 72.667 Million cell updates/sec
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1. /cgn2_6/ptodata/1/iaa/58 COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/68 COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcTUS COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcTUS COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcTUS COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcTUS COMB.pep:*
                                                                                                                                                                      1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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-08-930-777A-1
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-09-722-825-66
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                                                                                                                                                                                                                                          513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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238
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Perfect score:
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                                                                                       Run on:
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No.
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4, Appli	2, Appli	4, Appli	3, Appli	5, Appli	233, App	7, Appli	7, Appli	79	7, Appli	2, Appli	6, Appli	6, Appli	28, Appl	42632, A	163, App	7108, AE	6, Appli	
Sednence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	
US-08-487-359-4	US-08-222-798A-2	US-08-222-798A-4	US-09-024-975-3	US-08-930-777A-5	US-09-547-693-233	US-08-487-359-7	US-08-222-798A-7	US-09-949-016-7950	US-09-024-975-7	PCT-US95-12080-2	US-08-487-359-6	US-08-222-798A-6	US-09-917-340-28	US-09-270-767-42632	US-09-030-619-163	US-09-949-016-7108	US-08-930-777A-6	
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41.4	41.4	41.4	40.3	40.3	40.3	39.9	39.9	39.7	39.5	39.5	39.5	39.5	39.5	39.5	39.1	38.9	38.7	
98.5	98.5	98.5	96	96	96	95	95	94.5	94	9	94	94	94	94	93	92.5	92	
28	29	30	3.5	35	1 60	34	35	36	37	38	6.6	40	41	4.2	43	44	45	

#### ALIGNMENTS

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RESULT 1

US-08-125-052-1

US-08-125-052-1

US-08-125-052-1

Sequence 1, Application US/08162052

Parent No. 548575

GENERAL INFORMATION:

APPLICANT: BENAN, Hans G

APPLICANT: BORN, Hans G

ADDRESSES: Burns, Doane, Swecker & Mathis G

STREET: P.O. Box 1404

COUNTRY: United States

COUNTRY: United States

CONFUTER: TABLE FORM:

WINDIGH TYPE: FLOPPY disk

COMPUTER: TABLE FORM:

COMPUTER: TABLE COMPAT:

APPLICATION NUMBER: SE 9101838-2

FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9101838-2

FILING DATE: 23-DEC-1992

ATTORNEY AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 603300-299

TELECOMMUNICATION NUMBER: 6113

REFERENCE/DOCKET NUMBER: 6
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Length 39;

DB 1;

100.0%; Score 238;

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US-08-419-066-1
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                        Gaps
                                                                                                                                                                           US-08-310-722-1

Sequence 1, Application US/08310722

Patent No. S654273

GENERAL INFORMATION:

APPLICANT: Gallo, Richard L.

APPLICANT: Klagsbrun, Michael

TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
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                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRRPRPPYLPRPPPFFPPRLPPRIPPGFPPRFP 39
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                                                         1 RRRPRPPYLPRPRPPPRLPPRIPPGFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Lee, Jong-Youn AUTHORS: Lee, Jong-Youn AUTHORS: Mutt, Viktor AUTHORS: Jornvall, Hans TITLE: No. 5654273el Polypeptides And Their Use JOURNAL: PCT WO 92/22578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,722
  100.0%; Pred. No. 4.6e-17;
                                                                                                                                                                                                                                                                                                                                                             B: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1994
ON: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGIESTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (404)-815-6508
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.C
Matches 39; Conservative
                      39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
PUBLICATION INFORMATION:
Best Local Similarity
Matches 39; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Sequence 1, Application US/08419066 Patent No. 5830993

US-08-419-066-1

GENERAL INFORMATION:

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RESULT 4
US-08-728-333-1
; Sequence 1, Application US/08728333
; Patent No. 5863897
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Synducin Mediated Modulation of Tissue Repair
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; TUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; TREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                Hovey, Williams, Timmons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SIQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins, Hovey, Williams, Timmons
ADDRESSEE: Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kanasa City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,333
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP 39
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 238; DB 2;
Pred. No. 4.6e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AFFLICATION:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllina, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 2362
TELECOMMUNICATION INFORMATION:
TELEFAX: (816) 474-9057
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 39; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-930-777A-1
; Sequence 1, Application US/08930777A
; Patent No. 6713605
; GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Blecha, Frank
APPLICANT: Bli, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
TUTHER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Massouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: OCTOBER 8, 1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRRPREPRYLPREPREPERT 39
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100.0%; Score 239; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                           Query Match
100.0%; Score 238; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 50.0

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNATION: 530
ATTORNATION: 530
ATTORNATION: MAME: Collins, John M.
REGISTRATION NUMBER: 26,25-A
REFERENCE/DOCKET 1816, 474-9050
TELECOMMUNICATION INFORMATION:
TELEFRAX: (816) 474-9050
TELEFRAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-1
                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: BLECHA, FRANK
APPLICANT: SH, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 238; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels
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RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/024,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: No. 5863897el Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18 FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLING, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,722
FILING DATE: 22-SEP-1994
ATTONNEY/AGENT INTORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09024975
Patent No. 6133233
                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Bomen, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jornvall, Hans
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
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               Sequence 1, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Patrea L. Pabst
STREET: 2800 One Allantic Center
STREET: 1201 West Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1. Application US/09739535

Patent No. 6794490

GENERAL INFORMATION:

APPLICANT: Cubier Pharmaceuticals, Inc.

TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS

FILE REFERENCE: C060

CURRENT APPLICATION NUMBER: US/09/739,535

CURRENT FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/12080 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 238; DB 5;
100.0%; Pred. No. 4.6e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Novel Polypeptides And Their Use JOURNAL: PCT WO 92/22578
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DAIL.
CLASSIFICATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEPAX: (404)-815-8795
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
'FNGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jornvall, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic JS-09-739-535-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                 COUNTRY:
PCT-US95-12080-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-739-535-1
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APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: SHI, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
    Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.1%; Score 155; DB 2; Length 26; Best Local Similarity 100.0%; Pred. No. 3.7e-09; Matches 26; Conservative 0; Mismatches 0; Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Hovey, Williams, Timmons
                                                                                                                                                                                                                 US-08-419-066-2

Sequence 2, Application US/08419066

Patent No. 5830933

GENERAL INFORMATION:
APPLICANT: Blecha, Frank

APPLICANT: Blecha, Frank

TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins, Hovey, Williams, Timmons

ADDRESSEE: Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Kansas City
STATE: Ransas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
                                                                                                              1 RRRPRPPYLPRPRPPFFPPRLPPRIPP-FPPRFPP 38
    DB 4;
                                                                                         1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP
Score 221.5; DB 4,
Pred. No. 1.8e-15;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRRPRPPYLPRPRPPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
18-09-024-975-2
; Sequence 2, Application US/09024975
; Patent No. 6133233
  Query Match 93.1%;
Best Local Similarity 97.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal US-08-419-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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Query Match 58.8%; Score 140; DB 4; Length 23; Best Local Similarity 100.0%; Pred. No. 9.4e-08; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                       Length 26;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Blecha, Frank
APPLICANT: Blicha, Frank
APPLICANT: Bli, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR PAPLICATION NUMBER: PCT/US96/04674
FILING DATE: APTil 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 26; Conservative 0; Mismatches 0;
    NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                                                                                 4 PRPPYLPRPRPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08930777A Patent No. 6713605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-08-930-777A-3
                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
XGY: linear
                                                                                                                                                                                                                                                                  US-08-930-777A-2
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US-08-930-777A-3
                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08930777A
Patent No. 6713665
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MADIUM TYPER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATION STRIEM: C-DOS/NG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: TBM FC Compatible
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.1%; Score 155; DB 3; Best Local Similarity 100.0%; Pred. No. 3.7e-09 Matches 26; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                    1 RRRPRPPYLPRPRPPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-09-024-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                             ZIP: 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-930-777A-2
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Gaps

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Query Match

44.5%; Score 106; DB 1; Length 78;
Best Local Similarity 63.4%; Pred. No. 0.00058;
Matches 26; Conservative 0; Mismatches 7; Indels
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Patent No. 580453;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHER, ROBERT I.
TITLE OF INVENTION:
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 000 Pennsylvania Ave. N.W.
STREET: CA
COUWTRY: USA
COUWTRY: USA
COUWTRY: USA
COUWTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 PREPPPQEREPPPNFPGPRFP---PPQFPGPRFPPPFP 47
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ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FLING DATE: 07-JUN-1995
CLASSITCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H:
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEFRAK: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATOMOREY/AGENT INPOMMATION:

NAME:

NATANANISTRATION NUMBER:

ATOMOREY/AGENT INPOMMATION:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

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TELECOMMULICATION:

TELECOMMULICATION:

TELECOMMULICATION:

TELECOMMULICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 90-4030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-487-359-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-222-798A-5
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                                                                                                                                                                             US-08-950-777A-4-4

DS-08-950-777A-4-4

Patent No. 6713605

GENERAL INFORMATION:

TITLE OF INVERMINON: Synthetic Antimicrobial Peptide
APPLICANT: Shi, Jishu
TITLE OF INVERTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: Adol Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: April 10, 1996
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER: PCT/US6/04674
FILING DATE: April 10, 1996
CLASSIFICATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,263
REFERENCE/DOCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Preα....
100.0%; Mismatches
         1 PRPPYLPRPRPPFFPPRLPPRI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-487-359-5
; Sequence 5, Application US/08487359
; Patent No. 5633229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRRPRPPYLPRPRPPFFP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRRPRPPYLPRPRPPFFP 19
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CF
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-930-777A-4
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S.

8; Gaps

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SRQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
JOPOLOGY: linear
US-08-222-798A-5
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8; Gaps Query Match 44.5%; Score 106; DB 1; Length 78; Best Local Similarity 63.4%; Pred. No. 0.00058; Matches 26; Conservative 0; Mismatches 7; Indels

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4 PR--PPYLPRPR-PPPFFP-PRLPPRIPPGFP-PRFPPRFP 39

Search completed: October 26, 2005, 05:21:56 Job time : 42.0636 secs

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Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 18, Appl
Sequence 14, Appl
Sequence 20, Appl
Sequence 1, Appli
Sequence 1, Appli
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                                                                                                                                                                    October 26, 2005, 05:05:05; Search time 143.945 Seconds (without alignments) 113.119 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgm2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgm2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgm2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

5: /cgm2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

7: /cgm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

7: /cgm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

10: /cgm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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13: /cgm2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

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18: /cgm2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

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12: /cgm2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

13: /cgm2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

14: /cgm2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

15: /cgm2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                               1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP 39
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-391-155-1
US-10-391-155-2
US-10-651-147-1
US-10-651-147-1
US-10-916-185-14
US-10-991-286A-44
US-10-991-286A-44
US-09-739-742-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1862994 seqs, 417510619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Query
Match Length DB
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238
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100.0
100.0
100.0
100.0
100.0
93.1
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Perfect score:
Sequence:
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                                                                                                                       OM protein
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-10-01 -10-65 -10-01	-10-651-147-3 -10-437-963-19149	-10-437-963-	10-437-963-19189 10-014-147-4	-10-651-147-4	-10-437-963-13289	-10-425-115-20676	טר הינ	-10-437-963-17565	-10-437-963-20496	3-12096	-10-437-963-18013	-19189	3-	5-115-2	-10-437-963-1	-31607	3-1	-10-425-114-53570	-10-425-115-20231	a.	-10-437-963-17	-10-767-701-35371	US-10-425-115-289952	9-386-30	-10-424-599-14480	-10-424-599-2429	2
26 14 26 15 23 14						<del>.</del>	 		_		_	_	_			-	_	-	-	_	-		_	7		_	
	58.8	9.0	49.6	48.7	48.7	47.9	y . 7 4	46.6	46.6	10.5 46.4	46.4	109 45.8	45.4	45.4	45.0	45.0	44.5	44.5	44.5	44.5	44.5	05.5 44.3	.5 44.3	105 44.1		05 44.1	.5 43.9
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#### ALIGNMENTS

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US-10-014-147-1

Sequence 1, Application US/10014147

Sequence 1, Application US/10014147

Publication No. US20030125249A1

GENERAL INFORMATION:
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STRRET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City
STRATE: Massouri
COUNTRY: U.S.A.

ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: BC. 109
PRIOR APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: COLIUSE/O4674
FILING DATE: COLIUS, DADI M.
NAME: COLIUS, DOND M.
NAME: COLIUS, DOND M.
REPERENTING NUMBER: 25, 262
REFERENTING NUMBER: 23625-A
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US-10-391-155-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UCL.

ZIP: 01930

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 238; DB 14; Length 39; 100.0%; Pred. No. 8.1e-14; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 39;
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                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-014-147-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                               TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10391155 Publication No. US20040009463A1
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prasl
STREET: P.O. BOX 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Magnolia
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Best Local Similarity
Matches 39; Conserva
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RESULT 3

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                                                                                                                     TITLE OF INVENTION: Method for PR-39 peptide mediated selective inhibition of IKBA degradation
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                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRRPRPPYLPRPRPPPFPPRLPPRIPPGFPPRFP 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
RMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENČE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-391-155-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
Sequence 2, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simong, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 39 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Simons, Michael
                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 01930
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Magnolia
                                                                                                                                                                                                                                                                        CITY: Magnolia
                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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1 RRRPRPPYLPRPPFFPPRLPPRIPPGFPPRFP 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US2004/011829
PRIOR APPLICATION NUMBER: PCT/US2004/011829
PRIOR PILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/465,665
PRIOR PILING DATE: 2003-04-25
PRIOR PILING DATE: 2003-04-17
PRIOR PELING DATE: 2003-04-17
PRIOR PELING DATE: 2003-05-09
PRIOR PILING DATE: 2003-05-09
PRIOR PILING DATE: 2003-05-09
PRIOR PILING DATE: 2003-04-25
PRIOR PILING DATE: 2003-08-09
PRIOR PILING DATE: 2003-08-09
PRIOR PILING DATE: 2003-09-15
PRIOR PRILING DATE: 2003-09-15
PRIOR PILING DATE: 2003-09-15
PRIOR PRILING DATE: 2003-09-15
PRIOR PRILING DATE: 2003-09-15
PRIOR PILING DATE: 2003-09-15
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CURRENT FILING DATE: 2004-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Manoharan, Muthiah
APPLICANT: Kesavan, Venkitasamy
APPLICANT: Rajeev, Kallanthottathil G.
TITLE OF INVENTION: MODIFIED IRNA AGENTS
FILE REFERENCE: 14174-091001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/10916185
Publication No. US20050107325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-344-709C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 18
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TTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OCMPUTER: IBM PC compatible
OCMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CARDESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRPRPPYLPRPPPFFPPRLPPRIPPGFPPRFP 39
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Pred. No. 8.1e-14;
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100.0%; Pred. No. c...
0; Mismatches
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FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY AGENT INFORMATION:
NAME: Collins, John M.
                                                                                       INAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
APPLICATION NUMBER: US/10/391,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                    FILING DATE: 18-Mar-2003
CLASSIFICATION: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10651147 Publication No. US20040043934A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                  LENGTH: 39 amino acids
                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blecha, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 39; Conservative
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Sequence 18, Application US/10344709C
Sequence 18, Application US/10344709C
Sequence 18, Application US/10344709C
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JORG FRITZ ET AL.
TITLE OF INVERNION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVERNION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVERTION UNMERS: US/10/344,709C
CURRENT APPLICATION NUMBER: 2001-03-14
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
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     Length 39;
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                                                                                                                                            1 RRRPRPPYLPRPRPPFFFPRLPPRIPPGFPPRFPPRF 39
Query Match
100.0%; Score 238; DB 15;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 39; Conservative 0; Mismatches 0;
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US-09-739-535-1
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LENGTH: 38
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Publication No. US20050186591A1

GENERAL INFORMATION:

APPLICANT: Buncrot, David

APPLICANT: Barrer, Matthew J.

APPLICANT: Maragenore, Demerrius M.

APPLICANT: Warnchorer, Hans-Peter

ITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE

FILE REFRENCE: 1754 -003001

CURRENT APPLICATION NUMBER: US/10/991,286A

CURRENT APPLICATION NUMBER: US/10/991,286A

CURRENT APPLICATION NUMBER: US/004-11-17

PRIOR APPLICATION NUMBER: US 60/476,947

PRIOR FILING DATE: 2003-06-09

NUMBER OF SEQ ID NOS: 51

SOFTWARE FRAESEQ for Windows Version 4.0

SEQ ID NO 44
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 60/510,246
PRIOR FILING DATE: 2003-10-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 174
SOFTHARE: PastSEQ for Windows Version 4.0
LENGTH: 42
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                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Exemplary Cell Permeation Peptides US-10-916-185-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 238; DB 18;
100.0%; Pred. No. 8.6e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 238; DB 17;
100.0%; Pred. No. 8.6e-14;
tive 0; Mismatches 0;
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Publication No. US20050153337A1
GENERAL INFORMATION:
TITLE OF INVENTION: IRNA CONJUGATES
FILE REFERENCE: 14174-067001
CURRENT APPLICATION NUMBER: US/11/004,379
CURRENT FILING DATE: 2004-12-03
PRIOR PLICATION NUMBER: US CONTOR PRIOR APPLICATION NUMBER: PCT/US04/10586
PRIOR PILING DATE: 2004-04-05
PRIOR PLING DATE: 2004-04-05
PRIOR PILING DATE: 2004-04-05
                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 39; Conservative
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Matches 39; Conservative
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PRIOR APPLICATION NUMBER: US 60/462,894
PRIOR FILING DATE: 2003-04-14
PRIOR PLICATION NUMBER: US 60/465,665
PRIOR PLICATION NUMBER: US 60/463,772
PRIOR PAPLICATION NUMBER: US 60/469,612
PRIOR PAPLICATION NUMBER: US 60/469,612
PRIOR APPLICATION NUMBER: US 60/469,612
PRIOR PLING DATE: 2003-05-09
PRIOR FILING DATE: 2003-09-15
PRIOR FILING DATE: 2003-09-15
PRIOR PLING DATE: 2003-09-15
PRIOR FILING DATE: 2003-09-15
PRIOR FILING DATE: 2003-09-16
PRIOR FILING DATE: 2003-09-16
PRIOR FILING DATE: 2003-08-11
SEMBAINING PRIOR APPLICATION NUMBER: US 60/494,597
PRIOR FILING DATE: 2003-08-11
SEMBAINING PRIOR APPLICATION NUMBER: US 60/494,597
PRIOR FILING DATE: 2003-08-11
SEMBAINING PRIOR APPLICATION NUMBER: US 60/494,597
PRIOR FILING DATE: 2003-08-11
PRIOR OF SEQ ID NOS: 63
SEQ ID NOS: 63
FUNDATE: A PRIOR PRIOR APPLICATION NUMBER OF SEQ ID NOS: 63
FUNDATE: A PRIOR PRIOR APPLICATION NUMBER OF SEQ ID NOS: 63
FUNDATE: A PRIOR PRIOR APPLICATION NUMBER OF SEQ ID NOS: 63
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Sequence 1, Application US/09738742

Sequence 1, Application No. US20020025924A1

GENERAL INFORMATION:

APPLICANT: CLDist Pharmaceuticals, Inc.

APPLICANTION NUMBER: US/09/738,742

CURRENT FILING DATE: 2000-12-15

NUMBER OF SEQ ID NGS: 1

SOFTWARE: Patentin version 3.1
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APPLICANT INCUBATION:
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
FILE REFERENCE: C060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RRRPRPPYLPRPRPPFFPPRLPPRIPPGFPPRFPPRFP 39
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Publication No. US20020058785A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIE: 64108
UTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                          1 RRRPRPPYLPRPRPPPRLPPRIPPGFPPRFPPRFP 39
                                                                                                                                                                                                                                                                                                                                                                       1 RRRPRPATPATPATPPFFPPRLPPRIPP-FPPRFPP 38
                                                                                                                                                                                                                                                    Score 221.5; DB 9;
Pred. No. 2.1e-12;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/930,777A FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674 FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIPICATION: 530
CURRENT APPLICATION NUMBER: US/09/739,535
CURRENT FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 1
SCOTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 38
CAPPER: PRT
ORGANISM: Artificial
FRATURE:
FRATURE:
US-09-739-535-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10014147 Publication No. US20030125249A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEFAX: (816) 474-9057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Collins, John M
                                                                                                                                                                                                                                                           Query Match 93.1%;
Best Local Similarity 97.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-014-147-2
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Length 26;
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Sequence 3, Application US/20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: HOVEY, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                              Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: HOvey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.1%; Score 155; DB 15; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRILING DATE: 28-Aug-2003
CLASSIFICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APRIL 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COLLINE, JOHN M.
REFERENCE/DOCKET NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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Sequence 2, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (816) 474-90
TELEFAX: (816) 474-9057
                                                                                                                                                                                                                                                                                                                                 ZIP: 64108
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2
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STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-651-147-2
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0; Gaps

Length 23; Indels

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Ouery Match 58.8%; Score 140; DB 15; Best Local Similarity 100.0%; Pred. No. 1.3e-05; Matches 23; Conservative 0; Mismatches 0;
               REFERENCE/DOCKET NUMBER: 23625-A
                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 26, 2005, 05:28:55 Job time : 152.945 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PRPPYLPRPRPPFFPPRLPPRI 23
                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9057
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

FILING DATE: 07-DEC-2001

PRIOR APPLICATION NUMBER: US/08/930,777A

PRILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 474-9050

TELEPHONE: (916) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.8%; Score 140; DB 14; Length 23; Best Local Similarity 100.0%; Pred. No. 1.3e-05; Matches 23; Conservative 0; Mismatches 0; Indels
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COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COLIMB: A. 100 MARE: COLIMB: A. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-014-147-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-651-147-3
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 26, 2005, 04:51:43; Search time 102.345 Seconds (without alignments) 98.253 Million cell updates/sec Run on:

US-10-014-147-2

Perfect score: Sequence:

1 RRRPRPPYLPRPRPPPFFPPRLPPRI 26

Gapop 10.0 , Gapext: 0.5 **BLOSUM62** Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseq11980s: \*
geneseqp1990s: \*
geneseqp2000s: \*
geneseqp2001s: \*
geneseqp2001s: \*
geneseqp2003s: \*
geneseqp2003bs: \* A\_Geneseq\_16Dec04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description					•						PR-39	-	-					Aab51194 E. coli A		4	Adl67256 Antimicro	_	Ade86115 Proline-a	Adl67257 Antimicro	Aaw01448 Leukocyte
071777777777777777777777777777777777777	ID	AAW01447	AAW75723	ADE86113	ADL67255	AAR30491	AAR99121	AAR94446	AAW01446	AAW75722	AAB26888	AAB97280	AAB84690	ADD35364	ADE86112	ADL67254	ABB07714	ADR82250	AAB51194	AAW01451	ADE86114	ADL67256	AAW01452	ADE86115	ADL67257	AAW01448
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	Query Match Length	26	26	26	56	39	39	39	39	39	39	39	39	39	36	39	42	42	44	23	23	23	19	19	19	16
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.3	90.3	90.3	74.8	74 B	74.8	61.9
	Score	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	140	140	140	116	116	116	96
	Result No.	-	8		4	· w	9	7	α	σ.	10	11	15	13	14	. 55	16	17	α-	9 6	20	21	22	23	40	25

Prolin Prolin Antimi	Aab26885 PR-39 der Aab97277 PR-39 der Aab84691 Amino aci Aaw01450 Leukocyte		Aar79212 Bacteneci Aaw66400 Cationic Aay91699 Cationic Abu59576 Cationic	Ant J E. Rat	Aaw98069 Rat Fas 1 Aaw95040 Rat FasL Aa019029 Human Fas
AAW75724 ADB86116 ADL67258	AAB26885 AAB97277 AAB84691	AAW75725 ADE86118 ADL67260	AAR79212 AAW66400 AAY91699 ARI59576	ABB07713 AAB51197 AAR79095	AAW98069 AAW95040 AAO19029
2 60 60	W 4 4 C	4 CV 60 CC	2000	N 4 0	2 2 2
16 16 16	15	4 4 4 4	. W W W R	60 62 278	278 278 278
61.9 61.9 61.9	58.1 58.1			522.9	50.3
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26 27 28	939	4 6 6 6 4 6 4 9	, , , , , , , , , , , , , , , , , , ,	2 4 4 4 2 0 1 2	44 4 45 45

#### ALIGNMENTS

Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; byns synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy. Leukocyte O2- production inhibitor peptide PR26. AAW01447 standard; peptide; 26 AA. (first entry) 18-JUN-1997 Synthetic. AAW01447; RESULT 1 AAW01447 

96WO-US004674. 10-APR-1996; WO9632129-A1 17-0CT-1996.

(UNIV ) UNIV KANSAS STATE RES FOUND. 95US-00419066 10-APR-1995;

Shi J; Blecha F,

WPI; 1996-476842/47.

Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

Claim 3; Page 26; 45pp; English.

antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with but and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. These sequences, and PR39, can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (O2-) production. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte O2-

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The peptides can be used as medicaments for fighting

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definitistration into a mammal's bloodstream reduce repetitusion injury (production of reactive oxygen species, neutrophila deherence to endothellum, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXP, where P is a proline residue and X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arguine residues adjacent to these motifs, required for effective inhibition. It was established by structural and function analysis that a peptide should ideally contain 4 or 6 of these motifs, and that inhibitory activity is correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the neutrophil superoxide anion, and also the inhibition of neutrophil chemotaxis. From this, it was found that all of the peptides inhibit neutrophil oxidase to some extent. All of the peptides also inhibit neutrophil oxidase to some extent. All of the peptides also inhibit neutrophil oxidase activity. PR-39 is believed, to be the most potent endogenous produced, it can be suggested to be involved in eliminating or reducing the reperfusion injury induced adhesion and extraction of neutrophils.
                                                                                                                                                                                                    ö
                  infection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reduction of reperfusion injury in temporarily occluded blood vessels by administration of a peptide which is rich in proline or arginine
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                0; Indels
                                                                                                                                                       100.0%; Score 155; DB 2;
100.0%; Pred. No. 5.1e-09;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proline/Arginine rich peptide PR-26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 14-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                          AAW75723 standard; peptide; 26 AA
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                                                                               inflammatory disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-495359/42
                                                                                                                                                                          Similarity
                                                                                                                  Sequence 26 AA;
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Best Local S
Matches 26
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The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method of inhibiting leukocyte superoxide anion (02-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, a neutrophil, to a location, e.g. a wound site. The PR-rich peptides useful as medicaments to fight infection by attracting leukocytes to wound site, while restricting tissue damage at the wound site caused kecessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           administering peptide including peptide or its truncated analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                           Leukocyte superoxide anion; leukocyte O2- production,
leukocyte attraction; proline-arginine-rich antimicrobial peptide;
PR-rich antimicrobial peptide; neutrophil; wound site; infection;
tissue damage; oxygen radical; antibacterial.
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0
                                                                         Length 26;
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                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                   Proline-arginine (PR)-rich antimicrobial peptide PR-26.
                                                                      Score 155; DB 2;
Pred. No. 5.1e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 155; DB 8; 100.0%; Pred. No. 5.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 5.1
0; Mismatches
                                                                                                                                             1 RRRPRPPYLPRPRPPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attracting leukocyte to location by proline-arginine-rich antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRRPRPPYLPRPRPPFFPPRLPPRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 2; 24pp; English
                                                                                                                                                                                                                               ADE86113 standard; peptide; 26 AA
                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37-DEC-2001; 2001US-00014147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00419066.
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-059188/06.
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nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blecha F, Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003125249-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BLEC/) BLECHA
(SHIJ/) SHI J.
                                         Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1997;
                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                          ADE86113;
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Matches
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us-10-014-147-2.rag

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Indels

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Mismatches

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26; Conservative

Matches

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RESULT 5

AAR30491

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The invention relates to inhibiting leucocyte superoxide anion (02-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leucocytes with the peptide comprising 39 or 56 amino acids, for a time and under conditions effective to inhibit comprising services superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src composer to Analogy 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or porcine leucocyte and the mammalian leucocyte is neutrophil. Another comprise 16 control protein of a leo of selective peptide is at least 6 or 74 % of the total number of amino acids, where the sum of the proline and arginine residues in the condition of p47phox to p42phox in whole cells, therefore interfering with the binding to p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful to method as medicaments for fighting infections. The peptides are conditioned for find a medicaments for fighting infections by attreacting leucocytes to a wound site, yet restrict tissue danage at the wound site caused by consequence is PR-39 analog PR-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
                                                                                                                                                                    Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-26.

    .3
/note= "Essential for antibacterial activity"

                                                                                                                                                                                                                                                                                                                                                                   /note= "Essential for antibacterial activity"
                                                                                                                                  Antimicrobial peptide PR-39 analog PR-26
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2; 24pp; English
                    ADL67255 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00419066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2003; 2003US-00651147
                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blecha F, Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLEC/) BLECHA F.
                                                                                                                                                                                                                                                                                                                                                                                                           JS2004043934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1995;
08-OCT-1997;
                                                                                                                                                                                                                                                    Jnidentified
                                                                                              20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-2004
                                                        ADL67255;
                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                   Region
ADL6725!
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This peptide was isolated from the small intestine of a pig. The small inestine is an important endocrine organ and many physiologically active peptides have been isolated from it. This peptide inhibits the growth of, and may kill, bacteria, pref. gram negative bacteria. This peptide or its functional derivatives may be used in human or veterinary medicine for therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                     New anti-bacterial polypeptide - active against Gram negative bacteria.
                                                                                                     Pig; small intestine; endocrine; gram negative; bacteria; therapeutic; veterinary medicine; prophylactic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 155; DB 2;
100.0%; Pred. No. 7.2e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Joernvall H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRPRPPYLPRPPRPPRLPPRI 26
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AAR30491 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 10; 15pp; English.
                                                                                                                                                                                                                 92WO-SE000394
                                                                                                                                                                                                                                       91SE-00001838
                                                                                                                                                                                                                                                                                                                         Mutt V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1996 (first entry)
                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Conservative
                                                                                 Antibacterial peptide
                                                                                                                                           Sus scrofa domestica
                                                                                                                                                                                                                                                                                                   JOERNVALL H.
                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-018080/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                LEE J.
BOMAN H G.
                                                                                                                                                                                                                                                                                                                          Boman HG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39 AA;
                                                                                                                                                                                                                                         .4-JUN-1991;
                                                                                                                                                                                                                 10-JUN-1992;
                                                                                                                                                                  WO9222578-A1
                                                                                                                                                                                         23-DEC-1992.
                                              25-MAR-2003
12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR99121;
                        AAR30491;
                                                                                                                                                                                                                                                                           (BOMA/)
(MUTT/)
                                                                                                                                                                                                                                                                (LEEJ/)
                                                                                                                                                                                                                                                                                                    (JOER/)
                                                                                                                                                                                                                                                                                                                           Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Score 155; DB 8; Length 26; Pred. No. 5.1e-09;

100.0%;

Query Match Best Local Similarity

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Sequence 39 AA;
              22-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-0CT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                      Gallo RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blecha F,
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW01446;
                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                                                                                                          AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be used to treat sexually transmitted diseases (STDS) caused by Chlamydia, HIV, herpes simplex virus, Neisseria gonnorhoeae or Candida infection. The peptides inhibit STDS by either killing the infectious organism, impeding the infection mechanism or interrupting the replication cycle of the organism. Squalamine (an aminosterol host defence molecule of the dog fish shark Squalus acanthias) and PCLa (a frog antimicrobial peptide) analogues may also be useful in inhibiting STD infection and transmission
                                                                                                                                                                                                                                                  Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by administering magainin antimicrobial or squalamine cpd. to inhibit
STD; sexually transmitted disease; HIV; human immunodeficiency virus; herpes simplex virus; HSV; Neissería gonnorhoeae; Candida; Chlamydia; magainin; antimicrobial; squalamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synducin; induction; expression; syndecan-1; syndecan-4; surface; mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis; decubitus; ulcers; keloids; skin burns; ischemic tissues; hypercoagulation states; prevention; tumour metastasis; restenosis; inhibition, angiogenesis; proliferation; endothelial.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 155; DB 2; Length 39; 100.0%; Pred. No. 7.2e-09;
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                                                                                                                                                                                                            Bedi
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                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                          Example 1; Page 32; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR94446 standard; peptide; 39 AA.
                                                                                                                                                                                                          Williams T,
                                                                                   /note= "amidated"
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                                                                                                                                                95WO-US011675
                                                                                                                                                                    94US-00305475
                                                                                                                                                                                        (MAGA-) MAGAININ PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
                                                                                                                                                                                                           Zasloff M,
                                                                                                                                                                                                                              WPI; 1996-179725/18
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 39 AA;
                                                                Key
Modified-site
                                                                                                                                                                                                                                                                      transmission,
                                                                                                                                                13-SEP-1995;
                                                                                                                                                                    13-SEP-1994;
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                                                                                                        WO9608270-A2
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                                                                                                                           21-MAR-1996
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                                            Synthetic
                                                                                                                                                                                                            Jacob L,
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor; leukocyte 02- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; buts synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; supercoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
                                                                                                                                                                                                                                                                                                                                               Modulating mesenchymal interaction by administration of synducin - used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                       in the treatment of wounds, tumours, restenosis, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leukocyte O2- production inhibitor peptide PR39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 26; 34pp; English.
                                                                            (CHIL-) CHILDRENS MEDICAL CENT.
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94US-00310722.
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                                                                                                                                                                                                                                                      WPI; 1996-188401/19
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proline residue and X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was detablished by structural and function analysis that a peptide should ideally contain 4 or 6 of these motifs, and that inhibitory activity is correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the neutrophil superoxide annon, and also the inhibition of neutrophil chemotaxis. From this, it was found that all of the peptides inhibit neutrophil they oxidase to some extent. All of the peptides inhibit neutrophil down regulator of NADPH oxidase yet discovered, and from the data produced, it can be suggested to be involved in eliminating or reducing produced, in inno induced and extraction of neutrophiles.

the reperfusion injury induced adhesion and extraction of neutrophils. The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery

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Claim 2; Page 26; 45pp; English
                                         AAW75722;
                         Query Match
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Gaps

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0; Mismatches 56

Local Similarity 100.

Sequence 39 AA;

Query Match Matches

1 RRRPRPPYLPRPRPPFFPPRLPPRI

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Length 39; Indels

100.0%; Score 155; DB 2; 100.0%; Pred. No. 7.2e-09;

PR39. The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also inwound repair, showing that PR39 can be used in wound repair, as well on wound repair, showing that PR39 can be used in wound repair, as well on AAW01447-W01454, can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (O2-production. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte Q2-production. The peptides can be used as medicaments for fighting infection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating inflammatory disease states ö Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery. represents the proline-arginine rich antimicrobial peptide Gaps ö Length 39; Indels 100.0%; Score 155; DB 2; 100.0%; Pred. No. 7.2e-09; tive 0; Mismatches 0; 56 (UNIV ) UNIV KANSAS STATE RES FOUND. Proline/Arginine rich peptide PR-39. 1 RRRPRPPYLPRPRPPFFPPRLPPRI AAW75722 standard; peptide; 39 AA. 97US-00802306. 98WO-US003207 19-NOV-1998 (first entry) Best Local Similarity 100. Matches 26; Conservative Sequence 39 AA; 17-FEB-1998; 18-FEB-1997; 16-FEB-1998; WO9835690-A1 20-AUG-1998 Synthetic.

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This invention relates to a method for the stimulation of angiogenesis in situ within a targeted collection of viable cells. The method comprises introducing, into the cytoplasm, at least I member of the PR-39 eligopeptide collective, which interacts with cytoplasmic proteasomes. Part of the proteolytic activity of the proteosomes is selectively altered so as to stimulate angiogenesis. The method is used to induce angiogenesis in tissue that has suffered anoxia or infarction, e.g. myocardial infarction or chronic myocardial ischaemia, and also to study the mechanisms that control angiogenesis. The present sequence represents the PR-39 peptide from which peptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stimulating angiogenesis in situ, useful e.g. for treating anoxia and infarction, by administering a PR-39 oligopeptide that regulates enzymatic activity of proteosomes.
                                                                                                                                                              Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction; myocardial ischaemia; proteasome.
                                                                                                                                 PR-39 peptide used in angiogenesis control.
                                                                                                                                                                                                                                                                                                                                                                                          (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 21; 51pp; English
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                              AAB26888 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                        16-MAR-2000; 2000WO-US007050
                                                                                                                                                                                                                                                                                                                                                          99US-00276868
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-628319/60
                                                                                                                                                                                                                                                      WO200057895-A1
                                                                                                                                                                                                                                                                                                                                                              26-MAR-1999;
                                                                                                 01-FEB-2001
                                                                                                                                                                                                                                                                                        05-OCT-2000.
                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                               Simons M,
                                                                 AAB26888;
RESULT 10
                 AAB26888
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Sequences AAW75722-W75732 are proline/arginine rich peptides that upon administration into a mammal's bloodstream reduce reperfusion injury (production of reactive oxygen species, neutrophil adherence to endothelium, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXP, where P is a

Reduction of reperfusion injury in temporarily occluded blood vessels by administration of a peptide which is rich in proline or arginine

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Blecha F,

ковв СК,

WPI; 1998-495359/42

Claim 3; Page 14; 35pp; English

residues.

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Gaps

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Length 39; IndelB

Matches

SXS

RESULT 11 AAB97280

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The present sequence represents a PR-39 protein. The specification describes PR-39 derived peptides, which are used for selective inhibition of IxappaBalpha degradation within a targeted cell collection in-situ. The method is useful for selectively inhibiting IxappaBalpha protein degradation in situ, decreasing the activity of NFkappaB transcription factor and selective control of NFkappaB dependent gene expression in situ. The PR-39 derived peptides are useful in the treatment of myocardial infarction, chronic myocardial ischemia of heart disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selective inhibition of IkappaBalpha degradation within targeted viable cell collection, involves interacting PR-39 oligopeptide with IkappaBalpha and proteasomes, and altering proteolytic activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR-39; IkappaBalpha degradation; NFkappaB transcription factor; myocardial infarction; chronic myocardial ischemia; heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 100.0%; Score 155; DB 4; Length 39; Similarity 100.0%; Pred. No. 7.2e-09; 26; Conservative 0; Mismatches 0; Indels
  100.0%; Score 155; DB 4; 100.0%; Pred. No. 7.2e-09;
                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a PR-39 protein.
                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                               1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                           1 RRRPRPPYLPRPRPPPFFPPRLPPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 30; 69pp; English.
                                                                                                                                                                                                                                                               AAB84690 standard; protein; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-2000; 2000WO-US035293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00474967
                                                                                                                                                                                                                                                                                                                                                           17-SEP-2001 (first entry)
                                                 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-441690/47.
                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200147540-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteasomes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simons M,
                                                                                                                                                                                                                                                                                                            AAB84690;
Query Match
Best Local S
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Matches
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ADD35364
ID ADD35
XX
AC ADD35
XX
                                                 Matches
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ID AAB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39 is a member of the the cathelin family of proteins, mature PR-39 is a member of the the cathelin family of proteins, mature PR-39 is represented by the present sequence is 39 amino acids in length, and has been shown to play a role in several inflammatory events including wound healing and myocardial infarction. The PR-39 derived family of collgopeptides cause selective inhibition of proteasome mediated degeneration of peptides and stimulation of angiogenesis after their introduction to a target cell. PR-39 derived peptides are able to interact with at least the alpha7 subunit of the proteasomes, and therefore alter the proteolytic activity of proteasomes such that a selective increased expression of specific proteins occurs. The invention includes methods for the selective inhibition of proteasome mediated candidation. The method provides means for stimulating angiogenesis as required in living tissues and organs which have suffered defects or have undergone anoxia and/or infarction, myocardial infarction of cronic myocardial is schaemia of heart tissue. Examples are the myocardium, skeletal or smooth muscle, artery or vein, lung, brain, kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and extremities. A particular example is after myocardial infarction or
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stimulation of angiogenesis and inhibition of proteasome mediated degradation in cells, by introduction of PR-39 oligopeptide or its N-terminal fragments or their conjugates, for use in anoxia and infarction
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR-39; cathelin; inflammation; wound healing; myocardial infarction; proteasome; proteolysis; alpha7; peptide degradation; angiogenesis; anoxia; chronic myocardial ischaemia; heart tissue.
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0
                                                                                           100.0%; Score 155; DB 3; Length 39; 100.0%; Pred. No. 7.2e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                   1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                        AAB97280 standard; peptide; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00426011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2000; 2000WO-US027552
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-355179/37.
                                                                                                                 Local Similarity
les 26; Conserv
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                                                 Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200130368-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR-39 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
are derived
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                                                                                             Query Match
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Gaps

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ADD35364 standard; peptide; 39 AA.

ADD35364;

Sequence 39 AA;

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superoxide anion (02-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                                                                                                                                                                                                                                           Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs the location.
                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to a method of inhibiting leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leucocyte ; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil; infection; wound ; tissue damage ; PR-39 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Essential for antibacterial activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 155; DB 8;
100.0%; Pred. No. 7.2e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .14
|abel= PR-14_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .26
|abel= PR-26_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .19
|abel= PR-19_peptide
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/label= PR-23_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRRPRPPYLPRPRPPFFPPRLPPRI
                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL67254 standard; peptide; 39
                                                   07-DEC-2001; 2001US-00014147.
                                                                                       95US-00419066.
97US-00930777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptide PR-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 26; Conservative
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/label=
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                                                                                                                                                                                                                                          WPI; 2004-059188/06.
                                                                                                                                                                                                      Blecha F, Shi J;
                                                                                                                                              (BLEC/) BLECHA·F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jnidentified
                                                                                         10-APR-1995;
                                                                                                         08-OCT-1997;
               03-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intracoular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work spnergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocular cell dysplasia, iridial melanocyte hyperplasia, and hyperplamentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                       antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridan malanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leukocyte superoxide anion; leukocyte O2- production; leukocyte attraction; proline-arginine-rich antimicrobial peptide; PR-rich antimicrobial peptide; neutrophil; wound site; infection; tissue damage; oxygen radical; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proline-arginine (PR)-rich antimicrobial peptide PR-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 155; DB 8; 100.0%; Pred. No. 7.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 11; 11pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE86112 standard; peptide; 39
                                                                                                                                                                                                                                                                                     21-MAR-2003; 2003WO-US008935
                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002US-0367071P.
                                       Antimicrobial peptide PR-39
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   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                 (CAYM-) CAYMAN CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                      Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-011506/01
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Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003125249-A1
                                                                                                                                                                                                              WO2003079997-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention.
                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
   15-JAN-2004
                                                                                                                                                                                                                                                 02-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                      Maxey KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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RESULT 14 ADE86112

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Gaps

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Length 39; Indels

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Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
/note= "Essential for antibacterial activity"
25. .39
/label= PR-15_peptide
                                                                                                                                                                    Claim 1; SEQ ID NO 1; 24pp; English
                                                       28-AUG-2003; 2003US-00651147.
                                                                    95US-00419066.
                                                                                                                                                                                                                                                                                                                                  sequence is PR-39 peptide
                                                                                                                           WPI; 2004-225728/21.
                                                                                        (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                             Shi J;
                           US2004043934-A1.
                                                                    10-APR-1995;
08-OCT-1997;
                                         04-MAR-2004.
                                                                                                            Blecha F,
       Peptide
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The invention relates to inhibiting leucocyte superoxide anion (02-)

production using a naturally occurring proline-arginine (PR)-rich
antimicrobial peptide known as PR-39 and its truncated analogs. The
method comprises contacting leucocytes with the peptide comprising 39 or
26 amino acids, for a time and under conditions effective to inhibit
CC 16 amino acids, for a time and under conditions effective to inhibit
CC 26 amino acids, for a time and under conditions effective to inhibit
CC 16 amino acids, where the anion production, by binding to Src
CC 17 homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
CC 17 homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
CC 18 also disclosed which employs a PR-39 analog that comprise 16
method is also disclosed which employs a PR-39 analog that comprise 16
CC 26 amino acids, where the sum of the proline and arginine residues in the
CC 27 acids. This peptide is at least 66 or 74 % of the total number of amino
CC 27 production by the effective
CC 28 pinding to p47phox in whole cells, therefore interfering with the binding
CC 29 production are arginine residues. The method of the invention is useful
CC 20 proline are arginine residues. The method of the invention is useful
CC 20 parallel as medicaments for fighting infections by attracting leucocytes to
CC 20 a wound site, yet restrict tissue damage at the wound site caused by
CC 20 production is produced by these leucocytes. The present

Sequence 39 AA;

0; Gaps 100.0%; Score 155; DB 8; Length 39; 100.0%; Pred. No. 7.2e-09; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 26; Conservative

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Search completed: October 26, 2005, 05:12:04 Job time : 103.345 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 26, 2005, 05:00:14; Search time 19.3818 Seconds (without alignments) 129.071 Million cell updates/sec

US-10-014-147-2 155 I RRRPRPPYLPRPRPPFFPPRI 26 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ភ	Description	antimicrobial prot	hybrid proline-ric	bactenecin 7 - bov	extensin class I (	ı	Fas ligand - human	mucin-like protein	hypothetical prote	cathelin-like anti	earl	ដ	n U	2	bactenecin 5 precu	hypothetical prote	proline-rich prote	fibrillin-1 precur	extensin homolog -	prophenin (PF-2) p	proline-rich prote	hypothetical prote	gliadin - wheat	alpha/beta-gliadin	salivary protein F	proline-rich pepti	щ	_	_	hypothetical prote
SUMMAKIES	ID	568232	JQ1663	A36589	S14981	A49266	138707	T30351	G86292	\$57330	EDBEIF	\$51939	A34170	B36589	A45328	B40505	827200	A55624	T07176	S40463	T07598	T25073	A27319	S07361	S10782	PJHUSB	JC5572	S68230	T16159	T45564
	08	10	7	~	~	~	7	7	~	~	٦	~	Н	~	~	~	7	~	7	~	~	~	~	~	~	-1	7	7	~	0
	Length	172	301	59	199	278	281	1029	1006	212	1460	439	415	42	176	1958	389	2871	221	228	491	254	296	296	57	79	134	190	239	588
	% Query Match	100.0	54	52.9	51.6	50.3	49.7	48.7	48.4	48.1	47.4	47.1	46.5	46.1	46.1	46.1	45.2	45.2	44.8	44.8	44.8	44.5	44.5	•	•	•	43.9	43.9	•	43.9
	Score	155	84.5	82	80	78	77	. 75.5	75	74.5		73	72	71.5	71.5	71.5	70	70	69.5	69.5	σ	69	69	. 69		8	89	68	68	68
	Result No.	-	~	m	4	S	9	7	60	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	spore coat protein	hypothetical prote	proline-rich prote	probable coll wall	unknown protein Fl	cysteine-rich exte	hypothetical prote	cell wall protein	probable transcrip	proline-rich prote	hypothetical prote	gene msg1 protein	hypothetical prote	homeotic protein H	врlісеовоще-аввосі
T00074	A41051	D84672	839206	E71415	C96828	A48232	T13478	\$52985	T08599	T09792	T45867	S37485	T46446	B60492	A54964
~	~	N	~	N	~	N	~	~	7	~	7	~	0	٦	7
903	82	134	148	428	547	209	359	381	1098	299	508	147	246	251	424
43.9	43.5	43.5	43.5	43.5	43.5	43.2	43.2	43.2	43.2	42.9	42.9	42.6	42.6	42.6	42.6
89	67.5	67.5	67.5	67.5	67.5	67	67	67	67	66.5	66.5	99	99	99	99
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

	RESULT 1
	S68232 antimicrobial protein PR-39 precursor, cathelin-associated - pig
	N.Alternate names: myeloid antibacterial procein PK-39 C.spacies: Sus granda domestics (domestic pig)
	C, Detected 15-Pb-1997 #sequence review 13-Mar-1997 #text_change 09-Jul-2004
	C.ACCEBION: S002227 UNV033, 11,120, SIJJO3 R,Zhao, C.; Ganz, T.; Lehrer, R.I.
•	FEBS Lett. 376, 130-134, 1995 A.Titla. Structures of genes for two cathelin-associated antimicrobial peptides: propheni
	A; Reference number: S68232; MUID:96105365; PMID:7498526
	A;Accession: S68232 a.status. translation not shown
	A; Molecule type: DNA
	A;Residues: 1-172 ZZHA> a. rross-references: INTPROT:P80054: EMBL:X89201: NID:q1165150; PIDN:CAA61487.1; PID:g1165
	A, Experimental source: leukocytes
	R.Storici, P.; Zametti, M.
	BICCIENT IDEPLYS. THE SECOND THE STATE A SEQUENCE IDENTICAL TO THE I A. TITLE: A CINK derived from pig bone marrow cells predicts a sequence identical to the i
	A; Reference number: JN0899; MUID:94071853; PMID:8250863
	A; Accession: JN0899
	A MOLECULE CYPE: MKNA A Decidence 13-20 (2) 22-172 (STC)
	A: Cross-references: GB: L23825; NID: 9435100; PIDN: AAA31109.1; PID: 9435101
	R, Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome
	Proc. Natl. Addd. 201. U.S.A. yz. / UOS-'UOS' 1993 b.mitle. Structure of the gene for borgine bedidde antibiotic PR-39, a cathelin gene fami
	A; Reference number: 147138; MUID:95350216; PMID:7624374
	A; Accession: 147138
	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A MOLECULE TYPE: UNA A: Decembring
	A.Cross-references: EMBL:X87236; NID:q829142; PIDN:CAA60682.1; PID:g1051298
	R; Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,
	Bur. J. Blochem. 202, 849-884, 1991.
	A; Accession: S19563
	A; Molecule type: protein
	A; Residues: 131-169 < AGE>
	A;Experimental source: intestine
	Cydeneraca: Ayfane yra
	A; Introns: 66/3; 102/3; 126/3
	C; Superfamily: cathelin; cystatin homology
	C;Keywords: amidated carboxyl end; antibacceria.
	F:12-129/Domain: cystatin homology <cys.< td=""></cys.<>
	F;30-130/Domain: propeptide #etatus predicted <pro.< td=""></pro.<>
_	F,131-169/Froduct: antimicrobial protein Pr-39 #status experimental vent.

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-199 <SHO>
A;Cross-references: BMBL:X55692
A;Experimental source: cv. UC82B
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: cell wall; glycoprotein; hydroxyproline
                                                                                                                                                                                                         Score 80;
Pred. No.
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                                                                                                                                                                                                         51.6%;
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Best Local Similarity 60.9%
Matches 14, Conservative
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A;Accession: S57565
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Best Local Similarity
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A; Residues: 1-281 <MIT>
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A; Residues: 1-278 <SUD>
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A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
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R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
A;Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of A;Reference number: A36589; MUID:91035404; PMID:2229048
  F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1.301 <JOS>
A;Cross-references: UNIPROT:Q41848; EMBL:X60432; NID:g433706; PIDN:CAA42959.1; PID:g4337
A;Experimental source: strain W64A
C;Superfamily: hydroxyproline-rich glycoprotein
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R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response A;Reference number: S14970; MUID:91329690; PMID:1714316
A;Accession: S14981
                                                                                                                                                                                                                                                                                                                        hybrid proline-rich protein - maize
C;Species: Zea mays (maize)
C;Species: 30-69p-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1663
R;Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
Plant Cell 4, 413-423, 1992
A;Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein. A;Reference number: JQ1663; MuID:92361259; PMID:1498600
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C;Species: Lycopersicon esculentum (tomato)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                               ch 100.0%; Score 155; DB 2; Length 172; 1 Similarity 100.0%; Pred. No. 6e-09; 26; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 54.5%; Score 84.5; DB 2; Cocal Similarity 58.3%; Pred. No. 0.092; He 14; Conservative 3; Mismatches 4;
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                                                                                                                                                                                      1 RRRPRPPYLPRPRPPPFFPPRLPPRI 26
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A,Molecule type: protein
A,Residues: 1-59 <FRA
C,Superfamily: cathelin; cystatin homology
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                                                    Query Match
Best Local Similarity
Matches 26; Conserv
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A,Molecule type: mRNA
A,Residues: 1-281 -87ES-
A,Cross-references: UNIPROT: P48023; EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:959543
R,Mite, E.; Hayashi, N.; Ilo, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.;
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A,Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A,Reference number: JC2340; MUID:95071350; PMID:7980502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Call 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor A;Reference number: A49266; MUID:94084792; PMID:7505205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: P36940; GB: U03470; NID: 9440178; PIDN: AAC52129.1; PID: 9440179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 138707; JC2240, 557565; I38554
C;Accession: 138707; JC2240, 557565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity. A;Reference number: 138707; MUID:95127560; PMID:7826947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: D38122; DDBJ: D29820; NID: 9601892; PIDN: BAA07320.1; PID: 91369902
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                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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Length 199;
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   , DB 2;
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                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: glycoprotein; transmembrane protein
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submitted to the EMBL Data Library, June 1995
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A;Gene: FasL

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Nucleic Acids Res. 17, 4637-4646, 1989
A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies vir
A;Reference number: S04713; MUID:89315207; PMID:2546124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlternate names: antimicrobial peptide; prophenin-1
C;Species: Sus escreta domestica (domestic pig)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57330; S68726
R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacter
A;Reference number: S57330; MuID:96042752; PMID:7576250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-212 <STR>
A; Residues: 1-212 <STR>
A; Cross-references: UNIPROT: P51524; GB: X86031; NID: g1006756; PIDN: CAA60023.1; PID: g100675
R; Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I.
R; BEBS Lett. 362, 65-69, 1995
A; Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine le A;Reference number: S68726; MUID:95212585; PMID:7698355
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C;Species: suid herpesvirus 1
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04713
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                                                                                                                                                                       Gaps
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A;Residues: 1-1460 <CHE>
A;Cross-references: UNIPROT:P11675
C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 RRPRLRRQAFPPDNVPGPRFPPPNFPGPRFPP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 64 ;
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; Pred. No. 4.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RRPR-----PPYLPRPR-PPPFFP-PRLPP 24
                                                                                                      Score 75; DB 2
Pred. No. 2.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

48.1%; Score 74.5; D
Best Local Similarity 56.2%; Pred. No. 0.64
Matches 18; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 RORPGPPAAPGARPPP-OPPRPPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: leukocytes
C;Superfamily: cathelin; cystatin homology
C;Keywords: antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRRPRPPYLPRPRPPFFPPRLPP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: currents C; Keywords: antibacterial F; 6-113/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                      99 preparprepare--spare 117
                                                                                                                                                                                                                                        4 PRPPYLPRPRPPFFPPRLPP 24
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Best Local Similarity 62.5%;
Matches 15; Conservative
                                                                                                          48.4%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 131-209 < HAR>
                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S68726
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             C,Genetics:
A,Map position: 1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Molecule type: DNA
A;Roidues: 1-1006 (STO>
A;Cross-references: UNIPROT:Q9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdNNPV
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdNNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30351
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
V;rology 253, 17-34, 1999
V;rology 253, 17-34, 1999
V;riclogy 253, 17-34, 1999
V;riclogy 264, Disparsion of the genome of a baculovirus pathogenic for Lymantria d
A;Reference number: Z20836; MUID:99124785; PMID:9887315
                                               ő
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
B;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; U. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: 138554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 - RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
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C;Keywords: glycoprotesin; transmembrane protein
F:80-102/Domain: transmembrane #status predicted <TWM>
F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: DNA
A;Residues: 1-1029 <KUZ>
A;Cross-references: UNIPROT:Q9YMXO; EMBL:AF081810; PIDN:AAC70189.1
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Pred. No. 2.2;
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Best Local Similarity 62.5%; Pred. No. 0.47;
Matches 15; Conservative 1; Mismatches 8; Indels
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Matches

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chitinase (EC 3.2.1.14) precursor - beet

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A,Title: Zona pellucida binding of boar sperm acrosin is associated with the N-terminal I. A,Reference number: $10695; MUID:90306316; PMID:2365054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Activation of boar proacrosin is effected by processing at both N- and C-termine A;Reference number: S02780; MUID:89171246; PMID:2494060
A;Accession: S02780
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A, Residues: 17-29;34-66;88-91;94-121;123-166;171-184;190-207;209-216;219-228;231-245;248-
C, Superfamily: acrosin; trypsin homology
C, Superfamily: acrosin; trypsin homology
C, Reywords: glycoprotein; hydrolase; serine proteinase; sperm
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-415/Product: acrosin #status experimental <ADA'>
F;17-39/Product: acrosin light (A) chain #status experimental <ACH>
F;40-283/Domain: trypsin homology <TRX>
A, Note: the authors translated the codon CCT for residue 240 as Ala, GCC for residue 264
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C,Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-398,'KELL'
A; Cross-references: EMBL:X14844; NID:g1867; PIDN:CA32948.1; PID:g1868
A; Note: the difference at the carboxyl end is due to a frameshift error
R; Baba, T.; Michikawa, Y.; Kawakura, K.; Arai, Y.
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FEBS Lett. 265, 51-54, 1990
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FEBS Lett. 275, 139-142, 1990
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46.5%; Score 72; DB 1
Best Local Similarity 63.6%; Pred. No. 2.1;
Matches 14; Conservative 0; Mismatches
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                                                        R,Adham, I.M.
submitted to the EMBL Data Library, March 1989
A,Reference number: S16657
AA,Accession: S16657
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A;Residues: 1-42 <FRA>
C;Superfamily: cathelin; cystatin homology
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: protein A, Residues: 17-69 < BA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1, Residues: 40-62 <TO2>
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NiAlternate names: 53K fucose-binding protein
C;Species Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A34170; S08994; $02428; S04940; S16657; S02780; S10695; S12968
K;Baba, T.; Kashiwabara, S.; Watenabe, K.; Itch, H.; Michikawa, Y.; Kimura, K.; Takada, J. Biol. Chem. 264, 11920-11927, 1989
A;Title: Activation and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction and mechanisms of boar acrosin zymogen based on the deduction and maturation mechanisms of boar acrosin zymogen based on the deduction acrosin zymogen based on the deduction and maturation mechanisms and matur
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R;Residues: X', 10-25,'X',27-32,'X',34-38,'X',40-50 <CEC>
R;Residues: X',18,'X',18,'X',20-25,'X',34-38,'X',40-50 <CEC>
R;Residues: X',18,'X',18,'X',18,'X',10-15,'X',10-15,'X',40-50 < CEC>
FERS Lett. 226, 38-42, 1987
FERS Lett. 226, 38-42, 1987
A;Title: Acrosin shows zona and fucose binding, novel properties for a serine proteinase
A;Reference number: $02428; MUID:88083633; PMID:3480243
A;Accession: $02428
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A;Residues: 1-7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-393,'GN',396,'LVE',399-40
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                                                                                                                                                                                             C;Species: Beta vulgaris (beet)
C;Dates: 28-Oct.1996 #sequence revision 07-Peb-1997 #text_change 09-Jul-2004
C;Dates: 28-Oct.1996 #sequence revision 07-Peb-1997 #text_change 09-Jul-2004
C;Accession: SS1939; S7215; S45025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A. Plant Mol. Biol. 27, 211-216, 1995
A;Title: A proline-rich chitinase from Beta vulgaris.
A;Reference number: S51939; MUID:95170004; PMID:7865792
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R;Adham, I.M.; Klemm, U.; Maier, W.M.; Hoyer-Fender, S.; Tsaousidou, S.; Engel, W.
Eur. J. Biochem. 182, 563-568, 1989
A;Title: Molecular cloning of preproacrosin and analysis of its expression pattern in A;Reference number: $04940; MUID:89325301; PMID:2502391
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A,Residues: 1-439 cABEA
A,Gross-references: UNIPROT:Q42421, EMBL:X79301; NID:9488730; PID:9488731
A,Note: the authors translated the codon TGC for residue 416 as Gly
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Length 439; Indels

5,

47.1%; Score 73; DB; 66.7%; Pred. No. 1.8; 0; Mismatches

Query Match
Best Local Similarity 66.7
Matches 14; Conservative

114 PRPPPPTPRPPPPTPRPPP 134

a

24

4 PRPPYLPRPRPPPFFPPRLPP

A;Introns: 248/1; 300/2 C;Keywords: glycosidase; hydrolase F;1-25/Domain: signal sequence #status predicted <SIG> F;26-439/Product: chitinase #status predicted <MAT> F;26-439/Pomain: plant chitinase homology <PCH>

A,Molecule type: mRNA A,Residues: 191-397 <BER2>

C, Genetics:

A; Accession: S72315

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C;Accession: B36589
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
Biol. Chem. 265, 18871-18874, 1990
A;Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of A;Reference number: A36589; MUID:91035404; PMID:2229048
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A, Molecule type: protein

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-415 <BAB> A; Accession: A34170

7 RRPPIRPPEYPPERPPIRPPIRPP 34

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A,Molecule type: mRNA
A,Residues: 1-156 <ZANJ.
A,Residues: 1-156 <ZANJ.
A,Residues: 1-156 <ZANJ.
A,Crosa-references: UNIPROT.P19660; GB:L02650; NID:g162730; PIDN:AAA30404.1; PID:g162731
A,Crosa-references: UNIPROT.P19660; GB:L02650; NID:g162730; PIDN:AAA30404.1; PID:g162731
A;Note: sequence extracted from NCBI backbone (NCBIP:121443)
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; cystatin homology cCYS.
F;12-29/Domain: signal sequence #status predicted <SIG.
F;22-129/Domain: propeptide #status predicted <PRO.
F;30-130/Domain: propeptid # status predicted <PRO.
F;131-173/Product: neutrophil antibiotic protein Bac5 #status predicted <MAT.
F;131/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-1958 <CHE>
A, Ecrose-references: UNIPROT: Q69340, GB:M57505, NID:g334066; PIDN: AAA47468.1, PID:g334068
C, Superfamily: pseudorabies virus 1 nuclear antigen
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K.Cheung, A.K.
J. Virol. 65, 5260-5271, 1991
A.Title: Cloning of the latency gene and the early protein 0 gene of pseudorabies virus.
A.Reference number: A40505, MUID:91374576, PMID:1654441
                                                                                                                                                                                                                                   C;Accession: A45328
R;Zanetti, M.; Del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.
J. Biol. Chem. 268, 522-526, 1993
A;Title: The cDNA of the neutrophil antibiotic Bac5 predicts a pro-sequence homologous A;Eference number: A45328; MUD:93107055; PMID:8416958
A;Accession: A45328
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                                                                        bactenecin 5 precursor - bovine
NyAlternate names: Bac5, neutrophil antibiotic protein 5
C.Species: Bos primigenius taurus (cattle)
C.Species: Tr-Peb-1994 #sequence_revision 17-Peb-1994 #text_change 09-Jul-2004
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46.1%; Score 71.5; DB 2; Length 1958;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

46.1%; Score 71.5; DB 2; Length 176;
Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 16; Conservative 1; Mismatches 6; Indels
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RESULT 14
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2005, 04:52:03 ; Search time 90.0546 Seconds (without alignments) 147.844 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-014-147-2 155 1 RRRPRPPYLPRPRPPPFFPRLPPRI 26

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		_								P48023 homo sapien		oryza		09sbml volvox cart					Q7q3j9 anopheles g	homo	beta v	oryza	_		-		_	Q7sbd3 neurospora	bos taur	oryzias	Q8jht8 oryzias lat
SUMMARIES		ID	PR39 PIG	0E28 <u>Z</u> 0	041848	BCT7 BOVIN	Q6QTF1	Q9LV14	Q9XIZ3	TNF6 RAT	Q8S9B5	TNF6 HUMAN	07SC01	Q94JF6	094J98	Q9SBM1	Q9YMX0	Q9LMQ1	PF11_PIG	Q6ZD62	Q7Q3J9	096ЛН1	042421	Q6ESK7	065770	Q740X0	Q6F392	ACRO_PIG	096PN7	Q7SBD3	BCTS_BOVIN	P79817	08лнт8
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	ا ع	Match	100.0	55.2	54.5	52.9	52.3	52.3	51.0	50.3	50.0	49.7	49.7	49.4	49.0	49.0	48.7	48.4	48.1	48.1	48.1	47.7	47.1	47.1	46.8	46.8	46.5	46.5	46.5	46.5	46.1	46.1	46.1
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Q8j122 oryzias lat Q69j40 suid herpes Q99fw9 human papil Q948y7 volvox cart Q748p5 anopheles G Q74c95 geobacter G Q6zje9 oryza sativ Q9bdnl cercocebus Q8cgw4 mus museulu Q6sse6 chlamydomon Q82pc streptomyce Q84x72 chlamydomon Q86054 oryza sativ Q94513 cercopithec
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71.5 71.5 71.7 70.5 70.5 70.5 70.5 70.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

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Gaps

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SEQUENCE FROM N.A.
TISSUB-Bone marrow;
MEDLINE=95010016/0014-5793(94)00954-6;
SCOCCHI M., Romeo D., Zanetti M.;
"Molecular cloning of Bac7, a proline- and arginine-rich antimicrobial peptide from bovine neutrophils.";
FEBS Lett. 352:197-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=92361259; PubMed=1498600;
Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
"A maize embryo-specific gene encodes a proline-rich and hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-PRP;
Zea mays (Maize).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Vidiplantae; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 54.5%; Score 84.5; DB 2; Length 301; 1 Similarity 58.3%; Pred. No. 0.95; 14; Conservative 3; Mismatches 4; Indels 3
                                              55.2%; Score 85.5; DB 2; Length 228; 55.2%; Pred. No. 0.58; tive 3; Mismatches 5; Indels
228 AA; 24277 MW; EACA08812E410106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 AA; 31647 MW; 884EB70854D28C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
02-UUL-2004 (Rel. 44, Last annotation update)
Bactenecin 7 precursor (BAC7) (PR-59).
                                                                                                                                                                                                                                                                                                                                                              301 AA
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                                                                                                                                                              2 RRPRPPY----LPRPRPPPFFPPRLPPR 25
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                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                              Query Match
Best Local Similarity 55.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prolin rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCT7 BOVIN
P19661,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=BAC7;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Q41848
Q41848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT7_BOVIN
                                                                                                                                                                                                                                                                                                           RESULT 3
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                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMB. Outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
neutrophils that is analogous to PR-39, an antibacterial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                       the small intestine.";
J. Leukoc. Biol. 56:807-811(1994).
-!- FUNCTION: Exerts a potent antimicrobial activity against both E. coli and B. megaterium.
-!- TISSUE SPECIFICITY: Small intestine and bone marrow.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
Proline amide (G-170 provides amide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial protein PR-39. Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group)

G -> A (in Ref. 2).

A -> T (in Ref. 1).

RQ -> OR (in Ref. 1).

IHS -> NDP (in Ref. 1).

P -> I (in Ref. 5).

W; 994B792798COB133 CRC64;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004752; BAD07841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                EWBL; X87236; CAA66682.1; -.
EWBL; X89231; CAA61487.1; -.
PIRI; S88232; S68232.
HSSP, P32196; IKWI.
InterPro; IRR01894; Cathelicidin.
ProDom; P0001898; Cathelicidins; 1.
ProDom; P0001898; CATHELICIDINS_1;
PROSITE; PS00947; CATHELICIDINS_1;
PROSITE; PS00947; CATHELICIDINS_1;
PROSITE; P300947; CATHELICIDINS_1;
PROSITE; P300947; CATHELICIDINS_1;
PROSITE; P300947; CATHELICIDINS_1;
PROFITE; P300947; CATHELICIDINS_1;
PROFITE; P300947; CATHELICIDINS_1;
PYTOII done carboxylic acid; Signal.
SIGNAL 1 29 Potential.
PROPER 30 30 Antibacterial protein PIROPER 30 30 Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein P0501G04.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 RRRPRPPYLPRPRPPFFPPRL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19476 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Conservative
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29
90
117
157
172 AA;
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107
169
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MOD_RES
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CONFLICT
SEQUENCE
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Best Local
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Q62820;
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Matches

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RESULT 2

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Gaps

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Gaps

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Length 514;

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"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
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EMBL, AB020751; BAA97211.1; --
EMBL, AB010708; AA0116241; --
EMBL, BIO02708; AA0116241; --
EMBL, BIO02708; AA0116241; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MRG21 (AT5g62640/MRG21 6).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L., Ishida J., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Mirzanda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Torluni M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
euroaids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu B., Kotani H.,
                                                                                                                                                                                          SEQUENCE FROM N.A.
PubMed=15125772; DOI=10.1111/j.1365-313X.2004.02072.x;
PubMed=15125772; DOI=10.1111/j.1365-313X.2004.02072.x;
NOA Y.-S., Bizzell C.M., Noh B., Schomburg F.M., Amasino R.M., "EARLY FLOWERING 5 acts as a floral repressor in Arabidopsis." Plant J. 38:664-6722(2004).
EMBL, AVS26094; AAS19471.1; -
SEQUENCE 514 AA; 55467 MW; 04F230C24563BF2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               52.3%; Score 81; DB 2; 66.7%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 propygopogopomnepubb 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PRPPYLPRPRPPFFPPRLPP 24
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01-OCT-2000 (TrEMBLrel. 15,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 7:31-63(2000).
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                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q9LV14
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                   MEDLINE=91035404; PubMed=2229048; Prank R.W., Romeo D.; Prank R.W., Gennaro R., Schneider K., Przybylski M., Romeo D.; Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of bovine neutrophils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR01894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
Probom; PB001838; Cathelicidin; 1.
PROSTE; PS00946; CATHELICIDINS 1; 1.
PROSTE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Direct protein sequencing; Pyrrolidone carboxylic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         susceptible microorganisms.
-!- TISSUB SPECIFICITY: Large granules of neutrophils.
-!- PTM: Elastase is responsible for its maturation.
-!- MASS SPECTROMETRY: MW-18395; MW_ERR=1; METHOD=Electrospray; RANGE=30-190; NOTE=Ref.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrrolidone carboxylic acid.
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                                                   Scocchi M., Wang S., Zanetti M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21567 MW; 8CD07D7AA30A731C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Removed partially.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 AA
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                                                                                                                                            SEQUENCE OF 131-189, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bactenecin 7.
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
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                                                                                                                                                                                                                                                                                                                       . Biol. Chem. 265:18871-18874(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L42977; AAA87359.1; -.
EMBL; Y09471; CAA70616.1; -.
HSSP; P32196; 1KWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%;
68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGQTF1;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68..
Fra 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
130
190
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                                                                                                                                                                              IISSUE=Neutrophils;
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   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLY FLOWERING 5.
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PEPTIDE
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SIGNAL

PROPEP

Q6QTF1

SUPPLE

RESULT 5

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Name=1sq2
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CARBOHYD
CARBOHYD
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TRANSMEM
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                             Gaps
                                                                                                                                                                                                                         Ol-NOV-1999 (TrEMBLrel. 12, Created)
Ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-NOR-2004 (TrEMBLrel. 26, Last amnotation update)
Similar to Zea mays PRP gene. (X60432).
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 51.0%; Score 79; DB 2; Length 333; Local Similarity 50.0%; Pred. No. 3.5; Pred. 14; Conservative 3; Mismatches 9; Indels
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Nagamura Y., Yamamoto K.;
Submitted (FRB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB0034842: BAA78762.1; -.
HSSP; P24337; 1HYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; 02X123; -..
InterPro; IPR003612; AAI.
Pfam; PF00234; Tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
SEQUENCE 333 AA; 34823 MW; 268DEC74E20E8194 CRC64;
                         7;
                                                                                                                                                                                            333 AA
       66.7%; Pred. No. 3.5; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 RPPPTPPYVPSPPYVPPYIPPPYV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRRPRPPYLPRPRP--PPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Tnfsf6; Synonyms=Apt1Lg1, Fas1;
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                 378 РКРРУСРРЭСРРЭММКРРГРЭ 398
                                                              24
                                                              4 PRPPYLPRPRPPPFFPPRLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seqn
05-JUL-2004 (Rel. 44, Last anno
                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF6_RAT
ID TNF6_RAT
AC P36940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                            Q9XIZ3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tunor necrosis factor ligand superfamily member 6, membrane form.

Tunor necrosis factor ligand superfamily member 6, soluble form (By similarity).

Cytoplasmic (Potential).

Signal-anchor for type II membrane

Extracellular (Potential).
-!- TISSUE SPECIFICITY: Expressed in activated splenocytes and thymocytes. Moderate or weak expression found in small intestines, kidney and lung.
-!- INDUCTION: By PMA/ionomycin and concavalin/interleukin-2.
-!- PMM: The soluble form derives from the membrane form by proteolytic perocessing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Volvox carteri f. nagariensis.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvoxaceae; Volvox.
NCBI_TaxID=3068;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poly-Pro.
Cleavage (By similarity).
Potential.
N-linked (GICNAc. . .) (Potential).
N-linked (GICNAc. . .) (Potential).
N-linked (GICNAc. . .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2898E18A862CEAC6 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P50591; 1DG6.
RGD; 3880; Thfsf6.
InterPro; IPR008064; Fas_ligand.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006052; TNF Family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_like.
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PRINTS; PRO1234; TNECROSISECT.
PRODOM; PRO02012; TNF subf; 1.
SMART; SMO0207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31140 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A49266; A49266.
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257
278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00229; TNF;
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Best Local Similarity
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
(Apoptosis antigen ligand) (APTL) (CD178 antigen).
Name=TNFSFS Synonyms=APTLLG1, FASL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant of
                         STRAIN=HK10;
MEDLINE=21888633; PubMed=11891059; DOI=10.1016/S0378-1119(01)00899-X;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE PROM N.A. (ISOFORM 1).
MEDILNE-99127560; PubMed=7828947;
Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
"Human Fas ligand: gene structure, chromosomal location and species
                                                         Shimizu T., Inoue T., Shiraishi H., "Cloning and characterization of novel extensin-like cDNAs that are expressed during late somatic cell phase in the green alga Volvox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-955071350; PubMed-7980502;
MICH E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
Fusamoto H., Kamada T.,
"Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeytun A., Nagarkatti M., Nagarkatti P.S.;
"Isolation and characterization of a new naturally occuring varian
human Fas ligand that is expressed only in membrane bound form.";
Submitted (JUL-2000) to the EMBL/GenBank/DDB/ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E٦
                                                                                                                                                                                                                                                                                                   Score 77.5; DB 2; Length 625;
Pred. No. 8.9;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alderson M.;
"Fas ligand mediates activation-induced cell death in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            EMBL, AB070344; BAB65218.1; -.
InterPro; IPR008752; Peptidase_M1.
InterPro; IPR006025; Pept M Zn BS.
Pfam. PF05548; Peptidase M11; 1
PROSTIE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 625 AA; 67803 MW; 050420F8ABA013BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 204:468-474(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRPRPPYLPR-PRPPFFPPRLPPR 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95105731; PubMed=7528780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nt. Immunol. 6:1567-1574(1994)
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                                                                                                                                                                                                                                                                                      Cuery Match
Best Local Similarity 68.0%,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                             Gene 284:179-187(2002).
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A Table Standard B. A. Grouse L. H., Derge J. G., Strauberg R. L., Feingold E. A., Grouse L. H., Derge J. G., Strauberg R. L., Feingold E. A., Grouse L. H., Derge J. G., Schuler G. D., Strauberg R. L., Feingold E. A., Grouse L. H., Derge J. G., Schuler G. D., Atlachul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K., Appkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F., Diatchenko L., Marthaina K., Farmer A. A., Rubin G. M., Hong L., Rapleton M., Soares M. B., Ponaldo M. F., Casavint T. L., Scheet T. E., Rapleton M. J., Uddin T. B., Toshiyuki S., Carninci P., Prange C., Rap S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J., Robak S. A., McEwan P. J., Malek J. Hillon D. K., Warny D. M., Sodergren E. J., Iu X., Gibbs R. A., Richards S., Worley K. C., Hale S., Garcia A. M., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G., Shutterfield Y. S. N., Krzywinski M. I., Skalska U., Smailus D. E., Butterfield Y. S. N., Krzywinski M. I., Skalska U., Smailus D. E., All M. M. Marny D. M. A., Marra M. A., Schein J. E., Jones S. J. M., Marra M. A., Schein J. E., Jones S. J. M., Marra M. A., Schein J. E., Jones S. J. M., Marra M. A., Schein J. E., Marner M. A., Marra M. A., 
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DISEASE: Defects in TNFSF6 are a cause of autoimmune
DISEASE: Defects in TNFSF6 are a cause of autoimmune
DISEASE: Defects in TNFSF6 are a cause of autoimmune
DISEASE: Defects in TNFSF6 are a cail also known as
Canale-Smith syndrome (CSS). Aldes is a childhood syndrome
involving hemolytic anemia and thrombocytopenia with massive
Iymphadenopathy and splenomegaly.
SIMILARITY: Belongs to the tumor necrosis factor family.
DATABASE: NAME-EROW; NOTE-PROW 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
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Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
Wilkinson J.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
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ACOUNTY OF THE PROOFERS TO SEE THE PROOFERS TO SEE THE PROOFERS TO SEE THE PROOFERS This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor necrosis factor ligand superfamily member 6, membrane form.
Tumor necrosis factor ligand superfamily member 6, soluble form.
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP 006443.
Missing (In isoform 2).
FTId=VSP_00644
P-D,F.R: Lowers binding to TNFRSF6 and reduces cytotoxity more than 100-fold.
Y->F.R: Lowers binding to TNFRSF6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSOMHTASSL -> ATPVHPLKKRS (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abolishes cytotoxity. F->L: Abolishes binding to TNRFSF6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
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                                                                                                                                                                       EMBL; X89102; CAA61474.1; EMBL; U08137; AAC50071.1; EMBL; U11821; AAC50024.1; EMBL; D38122; BAA07320.1; EMBL; AF288573; AAG60017.1; EMBL; BC017502; AAH17502.1; EMBL; AB013303; BAA32542.1; -
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HSSP, PSOS91; 1D2Q.
Genew; HGNC:11936; TNFSF6.
H-InvDB; HIX0001337; -.
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A dalagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

Jaffe D., FitzHugh W., Man E.J., Smirnov S., Purcell S., Rehman B.,

Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulter B.,

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A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

A Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

A Cogoni C., Macino G., Catchenied D., Li W., Pratt R.J., Osmani S.A.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AABX01000145; EAA33970.1;
-- EMBL; BX842597; CAE75735.1;
HSSP; Q92831; 1JM4.
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Sordariomycetidae, Sordariales; Sordariaceae; Neurospora.
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PROSITE; PSS0014; BROMODOMAIN_2; 1.
Hypothetical protein.
SEQUENCE 1395 AA; 149956 WW; CB0D84322CDA8835 CRC64;
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Last sequence update)
Last annotation update)
                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
02-MAR-2004 (TrEMBLrel. 28, Last annotation update)
Predicted protein (Hypothetical protein B22K18.130)
Name=NCU09482.1; Synonyms=B22K18.130;
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                                  PRT; 1395 AA.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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Matches 13, Conservative
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                                    PRELIMINARY;
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Q94JF6;
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RESULT 11
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49.7%; Score 77; DB 1; Length 281; ilarity 62.5%; Pred. No. 4.5; Conservative 1; Mismatches 8; Indels

Query Match Best Local Similarity Matches 15; Conserv

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Yano M., Jiang J., Gojobori T.
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STRAIN=HK10;
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Q9YMX0
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Natik J. Apologozi B. Baba4025.1; -.
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SABBAIT, MATEURO N.A.
SABBAIT, MATEURO T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Nu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Nu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
No Samoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
N. Hijishita S., Honda M., Ichikawa Y., Itoh Y., Iwabuchi A., Kamiya K.,
N. Karaswa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Naraswa W., Machara T., Mizun H., Nakamichi Y., Nakamura M.,
Nagaski H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaswa K., Teuji K.,
Namiki N., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
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                 Name=P0684B02.12;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    44F6; -.
185 AA; 20609 MW; 57FF2D5645DEC4A3 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
02-DEC-2004 (TrEMBLrel. 28, Last annotation update)
P0047B08.14 protein (OJ1159 D09.5 protein).
Name=P0047B08.14; Synonyms=ÖJ1159_D09.5;
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Pubmed=12447438; DOI=10.1038/nature01184;
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                                                                                          NCBI_TaxID=39947;
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; CD0749C6AF02BD74 CRC64;
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"Response to the sexual pheromone and wounding in the green alga volvox: induction of an extracellular glycoprotein consisting almost exclusively of hydroxyproline.";
J. Biol. Chem. 274:35023-35028(1999).
EMBL, A3242246, CAB62280.1;
GO, GO:0005199; F:structural constituent of cell wall; IEA.
InterPro, IPR003882; Pistil extensin.
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Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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MEDLINE=99124785; Pubmed=9887315; DOI=10.1006/viro.1998.9469;
Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
"The genome sequence and structure of rice chromosome 1."; Marue 420:312-316 (2002).
EMBL; AP003053; BAB55690.1; -.
EMBL; AP003792; BAB89188.1; -.
                                                                                                                                                                    49.0%; Score 76; DB 2; Length 183; 51.5%; Pred. No. 3.7;
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Pred. No. 8.1;
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                                                                                                         14J98; -.
183 AA; 20155 MW; FICF823AD89CBB36 CRC64;
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09TMX-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SBM1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Hydroxyproline-rich glycoprotein DZ-HRGP precursor.
Name=HRGP gene;
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18 409 hy
409 AA; 41547 MW;
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Matches 14; Conservative
                                                                                                                                                                                                                            17; Conservative
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NCBI_TaxID=10449;
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NCBI_TaxID=3068;
                                                                                                                                                                                                  lest Local Similarity
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                                                                                                      Gramene; Q94J98;
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Slavicek J.M., Rohrmann G.F.;
"Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar.";
Virology 253:17-34(1999).
EMBL; ARC081810; AAC70189.1; -.
PIR; T30351; T30351.
SEQUENCE 1029 AA; 109195 MW; 61D8635EB6FADCC8 CRC64;
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Gaps 6; Indels 1; Query Match
Best Local Similarity 58.3%; Pred. No. 22;
Matches 14; Conservative 3; Mismatches 6; Indels 1; ò

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Search completed: October 26, 2005, 05:18:33 Job time : 93.0546 sec8

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1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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linear
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72.667 Million cell updates/sec
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Sequence 4, R
Sequence 4, R
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Sequence 1
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-930-777A-1

PCT-US-930-777A-3

US-08-930-777A-4

US-08-930-777A-4

US-08-930-777A-5
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US-08-930-777A-7
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1 RRRPRPPYLPRPRPPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                        513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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       Sequence 3, A
Sequence 8, A
Sequence 30,
Sequence 6, A
Sequence 10,
Sequence 11, A
Sequence 11, A
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Sequence 12,
Sequence 6, A
Sequence 6, A
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| Sequence 2, Application US/08419066
| Patent No. 5830993
| GENERAL INFORMATION:
| APPLICANT: Blacha, Frank
| APPLICANT: Blacha, Frank
| APPLICANT: Blacha, Frank
| APPLICANT: Blacha, Frank
| APPLICANT: AP
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
CLASSIFICATION: 530
ATYONRY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26262
REPERENCE/POCKET NUMBER: 26262
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (816) 474-9050
TELEPAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRAACTERISTICS:
TENTAME: 26 amino acids
US-09-479-524-3
US-08-339-214-8
US-08-339-214-8
US-09-3589-2878-6
US-09-157-864-10
US-09-005-7558-1
US-09-027-287-6
US-09-252-6568-6
US-09-258-6568-6
US-09-588-947A-6
US-09-588-2878-6
US-09-588-2878-6
US-09-588-2878-6
US-09-588-2878-6
US-09-658-6158-2
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US-09-507-968D-6
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-09-739-535-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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LENGTH: 38
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                                                                                                       Sequence 2, Application US/09024975
Sequence 2, Application US/09024975
Patent No. 613323
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: BLICHA, FRANK
INTILE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
COMMENT. MOD
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Sequence 2, Application US/08930777A
Sequence 3, Application US/08930777A
TITLE OF INVENTION:
MUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....LUNESSEE: HOVEY, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City STATE: Missouri COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
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1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 26; Conservative
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MOLECULE TYPE: peptide
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Gaps
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Patent No. 6794490
GENERAL INFORMATION:
APPLICANT: Cuber Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
FILE REFERENCE: C060
CURRENT APPLICATION NUMBER: US/09/739,535
CURRENT PILIG DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 155; DB 4; Length 26; Best Local Similarity 100.0%; Pred. No. 9e-10; Matches 26; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REPERENCE/DOCKET NUMBER: 26,262
REPERENCE/DOCKET NUMBER: 26,262
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
MUMBER: 26 aning acids
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US/08/310,722
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DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO:
                            ATTORNEY/AGENT INFORMATION:
NAME: Pabbet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCCZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NIMBER: 2626
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                       TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 Jornvall, Hans
                                                                                                                                                                                                                                                                                                                                                                              Lee, Jong-Your
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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Mutt, Viktor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Conservative
                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO PUBLICATION :
                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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                        FILING DATE: 2:
CLASSIFICATION:
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AUTHORS:
AUTHORS:
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US-08-419-066-1
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APPLICANT: Gallo, Richard L.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 39;
1.3e-09;
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                                JORNVALL, Hans
ENTION: NOVEL POLYPEPTIDES AND THEIR USE
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/162,052

FILING DATE: 02-JUN 1994

CLASSIFICATION NUMBER: US/08/162,052

FILING DATE: 02-JUN 1994

PRIOR APPLICATION NUMBER: SE 9101838-2

FILING DATE: 14-JUN-1991

PRIOR APPLICATION NUMBER: WO 92-22578

FILING DATE: 23-DEC-1992

ATTORNEY/AGENT INPORMATION:

NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
                                                                                           ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 155; Best Local Similarity 100.0%; Pred. No. 1 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                           ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08310722
Patent No. 5654273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 836-2021 PRORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 39 amino acids
                                                                                                                                                                 STATE: Virginia
COUNTRY: United States
          MUTT, Viktor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
          APPLICANT: MUTT, Vi
APPLICANT: JORNVALL
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY: USA
30309-4530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-162-052-1
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Gaps
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Sequence 1, Application US/08419066
Sequence 1, Application US/08419066
Sequence 1, Saloga
GENERAL INFORMATION:
APPLICANT: Shi, Jishu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: Collins, Hovey, Williams, Timmons
ADDRESSEE: Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: GA108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BR PC compatible
COMPUT
No. 5654273el Polypeptides And Their Use
.. PCT WO 92/22578
                                                                                                                                                                                                                             1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 155; DB 1;
100.0%; Pred. No. 1.3e-09;
tive 0; Mismatches 0;
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Query Match 100.0%; Score 155; DB 2; Length 39; Best Local Similarity 100.0%; Pred. No. 1.3e-09; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                            1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-930-777A-1
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US-09-024-975-1
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Sequence 1, Application US/08728333

Patent No. 5863897

GENERAL INFORMATION:
APPLICANT: Gallo, Richard L.
APPLICANT: Klagsbrun, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                100.0%; Score 155; DB 2; Length 39; 100.0%; Pred. No. 1.3e-09;
                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                              1 RRRPRPPYLPRPRPPFFPPRI 26
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,722
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L: PCT WO 92/22578
12/23/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Boman, Hans G. AUTHORS: Mutt, Viktor AUTHORS: Jornvall, Hans
                                                                                               HYPOTHETICAL: NO ;
ANTI-SENSE: NO ;
FRACHENT TYPE: N-terminal US-08-419-066-1
                                                                                                                                                                                                                                       26; Conservative
  39 amino acids
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                             NOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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US-08-728-333-1
LENGTH:
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Gaps
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Patent No. 6133233
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: BLICHO, DEPTIDE MODULATION OF REPERFUSION INJURY UNMER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY
CONTRACTOR OF THE ADDRESSES OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 155; DB 3; Length 39; 100.0%; Pred. No. 1.3e-09;
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLING, JOHN M.
REGISTRATION NUMBER: 25.262
REFERENCE/DOCKET NUMBER: 25.562
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1. Application US/08930777A
Patent No. 6713605
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blacha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Pept
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
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Gaps

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Sequence 3, Application US/08930777A;
Patent No. 6713605.
GENERAL INFORMATION:
APPLICANT: Bleche,
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
CORRESPONDENCES:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREE: 2405 Grand Blvd., Ste. 400
CITY: Kanasa City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Parentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 236.25-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.3%; Score 140; DB 4; L
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 155; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                 AUTHORS: Mutt, vin.
AUTHORS: Jornvall, Hans
TITLE: Novel Polypeptides And Their Use
TITLE: PCT WO 92/22578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (816) 474-9050
TELEPX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                      HYPOTHETICAL: NO ANTI-SENSE: NO PUBLICATION: AUTHORS: Lee, Jong-Youn AUTHORS: Boman, Hans GATHORS: Mutt, Viktor AUTHORS: Joinvall, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
linear
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US-08-930-777A-3
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Sequence 1, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES:
ACORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Allantic Center
STREET: 1201 West Peachtree
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                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THEN PC Compatible
COMPUTER: THEN PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0.8,1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 236.262
REFERENCE DOCKET NUMBER: 236.25-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER LETCS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USĀ

ZIP: 30109-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0;
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Kansas City
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TELEPHONE: (404)-813-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-930-777A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1201 Wes
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                     STATE: Missouri
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Gapa

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TOPOLOGY: linear
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US-08-930-777A-5
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Sequence 3, Application US/09024975

Sequence 3, Application US/09024975

Sequence 3, Application US/09024975

Betent No. 613323

GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: SHI JISHU
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400

CITY: KANSAS CITY

STATE: MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
74.8%; Score 116; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                             Patent No. 6713605

Patent No. 6713605

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

YUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALF: 04108
CALF: 04108
CAUPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: PS-1096
CLASSIFICATION NUMBER: 230
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 2, 26, 262
REFERENCE/DOCKET NUMBER: 2, 26, 262
REFERENCE/DOCKET NUMBER: 2, 23625-A
TELEFAM: (816) 474-9050
TELEFAM: (816) 474-9050
TELEFAM: (816) 474-9050
TELEFAM: 18 amino acids
LENGTH: 19 amino acids
TWOD: AMINO ACID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
1 PRPPYLPRPRPPFFPPRLPPRI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRRPRPPYLPRPRPPFFP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                        -08-930-777A-4
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Query Match 61.9%; Score 96; DB 4; Length 16; Best Local Similarity 100.0%; Pred. No. 0.00052; Matches 16; Conservative 0; Mismatches 0; Indels
; INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide US-08-930-777A-5
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Š 셤 Search completed: October 26, 2005, 05:21:57 Job time : 27.7091 secs

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Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 2, Appli
Sequence 6, Appli
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                                                                                                                                           October 26, 2005, 05:05:05; Search time 95.9636 Seconds (without alignments) 113.119 Million cell updates/sec
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Sequence 18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/NGT7 PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NGO_REW_PUB.pep:*
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22: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-788-742-1
US-09-738-742-1
US-10-014-147-1
US-10-31-155-1
US-10-391-155-2
US-10-391-155-6
US-10-391-155-6
US-10-31-155-6
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                                                                                                                                                                                                                                                                                                                                                                                                               1862994 segs, 417510619 residues
                                                                                                                                                                                                                                                                                           1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Query
Match Length DB
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155
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Perfect score:
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                                                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                  Run on:
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Sequence 44, Appl Sequence 20, Appl Sequence 3, Appli Sequence 3, Appli	equence				Sequence 19539, A								ø		Sequence	Sednence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	equence	Sequence 316071,	26764	Sequence 51171, A
US-10-991-286 US-11-004-379 US-10-014-147 US-10-651-147	US-1( US-1)	US-10-014-147	US-1(	US-10-39	US-10	US-10-42	US-10-42	US-10-42	US-10-01	US-1	US-10-43	US-10-43	US-10-437-963-13289	~	US-09-912-609-51	US-10-277-23	US-1	US-10-425-115	US-10-425-115-31607	US-10-424-599-2676	US-10-767-701-511						
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24 4 2 2 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	15151	7, 7	6	16	200	322	183	24	17	1,	86	192	276	55	Š	55	55	5.0	9	æ	48	16	17	25	287	10	13;
100.0 100.0 90.3	74.8	61.9	58.7	58.1	55.8	54.5	54.2	53.9	53.5	53.5	53.5	53.5	53.2	52.9	52.9	52.9	52.9	52.9	52.9	52.6	52.6	52.3	52.3	51.9	51.9	51.6	51.6
155 155 140	116	96	91	06	89.5	84.5	84	83.5	83	83	83	83	82.5	82	82	82	82	82	82	٠	81.5	В	81	°.	80.5	80	80
113	16	118	202	21	23 23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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RESULT 1

Sequence 2, Application US/10014147

Sequence 2. Application US/10014147

Publication No US20030125249A1

GENERAL INFORMATION:

TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City
STRATE: 1405 Grand Blvd., Ste. 400

CITY: Kansas City
STRATE: 1009 disk

COMPUTER: N.S.A.

COMPUTER: ELADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

FILING DATE: October 8, 1997

APPLICATION NUMBER: US/08/930;777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION:

NAME: COllins, John M.

REFERENCE/DOCKET NUMBER: 256.262
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1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-09-738-742-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                        RESULT 3
US-09-738-742-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-014-147-1
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LENGIH: 38
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                                                                                                                                                                                                                                   / Match 100.0%; Score 155; DB 14; Length 26; Local Similarity 100.0%; Pred. No. 7.7e-08; Los 26; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 155; DB 15;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 26; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APFLI 10, 1996
ATTORNEY/ARGNT INFORMATION:
NAME: COllins, John M:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-651-147-2
                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                      1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                            1 RREPREPYLPRPRPPPPRLPPRI 26
                TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (816) 474-9050
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10651147 Publication No. US20040043934A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (816) 474-9057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-651-147-2
                                                                                                                                                                                                                                           Query Match
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Publication No. US2002005898541

GENERAL INFORMATION:

APPLICANT: Cubist Pharmaceuticals, Inc.

TITLE OF INVENTION: NUMBER: US/09/739,535

CURRENT FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTH: 38
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Sequence 1, Application US/09738742
Publication No. US20020025924A1
GRNERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
APPLICANT: Cubist Pharmaceuticals, Inc.
APPLICANT: Cubist Pharmaceuticals, Inc.
FITER REFERENCE: C060
CURRENT APPLICATION NUMBER: US/09/738,742
CURRENT PILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 155; DB 9; Length 38; 1 Similarity 100.0%; Pred. No. 1.1e-07; 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 38;
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TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDERSSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 155; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 26; Conservative 0; Mismatches 0;
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Gaps
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TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUCUMITER D1930

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
COMPUTER: Dell PC
OPERATING SYSTEM: MS XP
SOFFMARE: WordPerfect version 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18 -Mar-2003
CLASSIFICATION: Unknown
ATTORNEY/AGRNT INPORMATION:
NAME: David Prashker, ESq.
REGISTRATION NUMBER: 29,693
REGISTRATION NUMBER: 29,693
REGISTRATION NUMBER: 39,693
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 10 S25-3794
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 155; DB 15; Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simons, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Magnolia
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-391-155-2
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GAO, Youhe
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
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                                                                                                                      COMPUTER FIOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

PILING DATE: 07-Dec-2001

CLASSIFICATION S30

PRIOR APPLICATION DATE: PCT/US96/04674

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLI 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: COllins, John M.

REGISTRATION NUMBER: 25,262

REFERENCE/DOCKET: NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-044/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RREPREPETURE 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-10-391-155-1
Sequence 1, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simons, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 01930
COMPUTER READABLE FORM:
                                                                              ZIP: 64108
COMPUTER READABLE FORM:
              CITY: Kansas City
                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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US-10-916-185-14
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                Sequence 6, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
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                                                                                                                                                                                                                                                                                                                                   ZIP: 10130
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS XP
OPERATING SYSTEM: MS XP
OPERATING SYSTEM: WITH A SOFTWARE: WORDERFECT VETSION 10
CURRENT APPLICATION DATA:
FILING DATE: 18-Mar-2003
CLASSIFICATION: UNknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blecha, Frank
Shi, Jishu
TILLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400
STREET: Kansas City
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 155; DB 15; Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: David Preshker, Esq.
REGISTRATION NUMBER: 29,693
REGISTRATION NUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
                                                                                                                                                                                                  CORRESPONDENČE ADDRESS:
ADDRESSEE: David Prashker, Esg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRPRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 39 amino acids
                                                                                                                                                                                                                                                 STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                      CITY: Magnolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-651-147-1
US-10-391-155-6
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US-10-344-709C-18

US-10-344-709C-18

US-10-344-709C-18

US-10-344-709C-18

US-10-344-709C-18

Sequence 18, Application US/10344709C

Publication No. US20040170642A1

GENERAL INFORMATION:

APPLICANT: JORG FRITZ ET AL.

TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

CURRENT FILING DATE: 2003-02-14

FILE REFERENCE: SONN:0303-02-14

FRIOR PILING DATE: 2001-08-17

PRIOR PLING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Pred. No. 1.2e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 155; DB 15;
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0;
                                                                FILING DATE: OCCODER 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APTI1 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET UNBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELECHONE: (816) 474-9050
TELEFAX: (816) 474-9057
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRRPRPPYLPRPRPPPFFPPRLPPRI 26
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Publication No. US20050107325A1
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Kesavan, Venkitasamy
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 26; Conservative
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Best Local Similarity 100.0
Matches 26; Conservative
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Gaps
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                                      Indels
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Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Exemplary Cell Permeation Peptides US-11-004-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 26; Conservative 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 1.2e-07; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARLAL INFORMATION:

CHARLAL INFORMATION:

TITLE OF INVENTION: IRNA CONJUGATES

FILE REFERENCE: 14174-067001

CURRENT PEDILGATION NUMBER: US/11/004,379

CURRENT PELING DATE: 2004-12-03

PRIOR PELING DATE: 2004-06-05

PRIOR FILING DATE: 2003-04-05

PRIOR FILING DATE: 2003-04-14

PRIOR FILING DATE: 2003-04-14

PRIOR FILING DATE: 2003-04-14

PRIOR FILING DATE: 2003-04-14

PRIOR FILING DATE: 2003-04-17

PRIOR FILING DATE: 2003-09-15

PRIOR FILING DATE: 2003-09-16

PRIOR FILING DATE: 2003-08-08

PRIOR PILING DATE: 2003-08-08

PRIOR FILING DATE: 2003-08-08

PRIOR PILING DATE: 2003-08-08

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                                                                                                                                                           1 RRRPRPPYLPRPRPPFFPPRLPPRI
                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/11004379 Publication No. US20050153337A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
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STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                         US-11-004-379-20
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LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENCTH: 42
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; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-916-185-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Exemplary Cell Permeation Peptide US-10-991-286A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 155; DB 17; Best Local Similarity 100.0%; Pred. No. 1.2e-07; Matches 26; Conservative 0; Mismatches 0;
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APPLICANT: Rajeev, Kallanthottathil G.
TITLE OF INVENTION: MODIFIED IRNA AGENTS
FILE REFRENCES: 14174-09101
CURRENT APPLICATION NUMBER: US/10/916,185
CURRENT FILING DATE: 2004-08-10
PRIOR PELING DATE: 2004-04-16
PRIOR PILING DATE: 2003-04-16
PRIOR PILING DATE: 2003-04-16
PRIOR PILING DATE: 2003-04-16
PRIOR PILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-05-09
PRIOR PILING DATE: 2003-06-09
PRIOR PILING DATE: 2003-06-09
PRIOR PILING DATE: 2003-06-08
PRIOR PILING DATE: 2003-06-08
PRIOR PILING DATE: 2003-06-08
PRIOR PILING DATE: 2003-08-11
PRIOR PILING DATE: 2003-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-991-286A-44
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

FILING DATE: 07-Dec-2001

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PT/US96,04674

FILING DATE: April 10, 1996

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 26,262

TELECOMMUNICATION INFORMATION:

TOWN INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.3%; Score 140; DB 14; Length 23; Best Local Similarity 100.0%; Pred. No. 1.7e-06; Matches 23; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BE PC COMPATION

SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/651,147

FILING DATE: 28-Aug-2003

CLASSIFICATION NUMBER: US/08/930,777A

RILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION NUMBER: PCT/US96/04674

ATTORNEY/AGENT INFORMATION:

NAME: COLIDIES, JOHN M.

NAME: COLIDIES, JOHN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PRPPYLPRPRPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acids
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US-10-651-147-3
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us-10-014-147-5.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 26, 2005, 04:51:43; Search time 62.9818 Seconds (without alignments) 98.253 Million cell updates/sec Run on:

US-10-014-147-5 96 Title: . Perfect score:

1 RPRPPFFPPRLPPRI 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2000s:\*
5: geneseqp201s:\*
6: geneseqp2002s:\*
7: geneseqp2003bs:\*
7: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw01448 Leukocyte											-					PR-39	_	Amino		_		-	8	Aab51194 E. coli A
SUMMARIES	· OI	AAW01448	AAW75724	ADE86116	ADL67258	AAW01451	ADE86114	ADL67256	AAW01447	AAW75723	ADE86113	ADL67255	AAR30491	AAR99121	AAR94446	AAW01446	AAW75722	AAB26888	AAB97280	AAB84690	ADD35364	ADE86112	ADL67254	ABB07714	ADR82250	AAB51194
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	Length	16	16	16	16	23	23	23	26	26	26	26	39	39	39	39	39	39	39	39	39	39	39	42	42	44
•	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100:0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96
	Result No.		8	m	4	S	φ	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aay17387 Human DNA Abu52849 Human ute Aaw14802 Human sec Abc95252 Human nov	Region Novel Human		Aay72162 Human RNA Adg96576 T cell ac Aau15847 Human nov Abu54916 Human nov	Human Human Protei	Abbso177 Human tra Adb64690 Human pro Adc31185 Human nov
AAY17387 ABU52849 AAW74802	ABG95252 ABG34446 ADI23107 ADH74109	AAB56895 ADC31125 AAM78694	AAY72162 ADQ96576 AAU15847	AAU16308 ABU55377 AAY02613	ABB50177 ADB64690 ADC31185
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## ALIGNMENTS

Leukocyte 02- production inhibitor peptide PR16. Ź AAW01448 standard; peptide; 16 (first entry) 18-JUN-1997 AAW01448; RESULT 1 AAW01448 

Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; byns synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; supercoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.

Synthetic.

WO9632129-A1

17-0CT-1996.

96WO-US004674. 10-APR-1996;

95US-00419066. 10-APR-1995; (UNIV ) UNIV KANSAS STATE RES FOUND.

Shi J; Blecha F,

WPI; 1996-476842/47.

Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39,

Claim 12; Page 28; 45pp; English.

AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. These sequences, and PR39, can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (O2-) production. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte 02-

The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery

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Gaps

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Indels Length

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100.0%; Score 96; DB 2; I 100.0%; Pred. No. 0.00017; Mismatches

.. 0

Query Match Best Local Similarity 100. Matches 16; Conservative

Sequence 16 AA;

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definition into a mammal's bloodstream reduce reperfusion injury of preduction of reactive oxygen species, neutrophil adherence to condiction of reactive oxygen species, neutrophil adherence to requirements: they contain the consensus sequence PXXP, where P is a requirements: they contain the consensus sequence PXXP, where P is a problem of is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was adjacent to these motifs, required for effective inhibition. It was established by structural and function analysis that a peptide should ideally contain 4 or 6 of these motifs, and that inhibition of the correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the neutrophil chemotaxis. From this, it was found that all of the peptides inhibit and NADPH oxidase to some extent. All of the peptides also inhibit neutrophil oxidase to some extent. All of the peptides also inhibit neutrophil oxidase activity. PR-39 is believed, to be the most potent endogenous produced, it can be suggested to be involved in eliminating or reducing the reperfusion injury induced adhesion and extraction of neutrophils.
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production. The peptides can be used as medicaments for fighting infection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reduction of reperfusion injury in temporarily occluded blood vessels by administration of a peptide which is rich in proline or arginine
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                    ö
                                                                                                                                                             Length 16;
                                                                                                                                                                                                0; Indels
                                                                                                                                                         Score 96; DB 2; I
Pred. No. 0.00017;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                              AAW75724 standard; peptide; 16 AA.
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                                                                                                                                                           100.0%;
100.0%;
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                                                                                                                                                                                                                                                             97US-00802306
98US-00024975
                                                                               inflammatory disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                     1 RPRPPFFPPRLPPRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-495359/42.
                                                                                                                  Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW75724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method of inhibiting leukocyte
                                                                                                                                                                                                                        Leukocyte superoxide anion; leukocyte O2- production;
leukocyte attraction; proline-arginine-rich antimicrobial peptide;
PR-rich antimicrobial peptide; neutrophil; wound site; infection;
tissue damage; oxygen radical; antibacterial.
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                                                                                                                                                                                                 Proline-arginine (PR)-rich antimicrobial peptide PR-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 5; 24pp; English.
                                                                                                       ADE86116 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-2001; 2001US-00014147.
                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00419066.
               1 RPRPPPFPPRLPPRI 16
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                                                                                                                                                                  (first entry)
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Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-059188/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the location.
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                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                     ADE86116;
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Matches
                                                                          RESULT 3
                                                                                          ADE86116
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Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; bank synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.

Leukocyte O2- production inhibitor peptide PR23.

18-JUN-1997 (first entry)

AAW01451;

AAW01451 standard; peptide; 23 AA.

RESULT S

AAW01451

us-10-014-147-5.rag

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The invention relates to inhibiting leucocyte superoxide anion (02-)
production using a naturally occurring proline-arginine (PR)-rich
antimicrobial peptide known as PR-39 and its truncated analogs. The
antimicrobial peptide known as PR-39 and its truncated analogs. The
cathod comprises contacting leucocytes with the peptide comprising 39 or
CC 66 amino acids, for a time and under conditions effective to inhibit
cof NADPH oxidase responsible for anion production, by binding to Src
chomology 3 (SH3) domain of p47phox, which is a 47 kDa cycosolic protein
cof the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or
cof the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or
cof the phagocytic sat least 6 cor 74 % of the total number of amino
acids, where the sum of the proline and arginine residues in the
cffective peptide is at least 6 for 74 % of the total number of amino
acids. This peptide inhibits leucocyte 02-production by the effective
binding to p47phox in whole cells, therefore interfering with the binding
cc of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
c the peptide are arginine residues. The method of the invention is useful
cof inhibiting leucocyte oxygen radical production. The peptides are
cof a wound site, yet restrict tissue damage at the wound site caused by
cexcessive oxygen radicals produced by these leucocytes. The present
cc sequence is PR-39 analog, PR-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
                                                                                                                                                                                         Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-16.
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Pred. No. 0.00017;
                                                                                                                                                         Antimicrobial peptide PR-39 analog PR-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 5; 24pp; English
                                        ADL67258 standard; peptide; 16 AA.
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100.0%;
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-225728/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shi J;
                                                                                                                                                                                                                                                                                                                  US2004043934-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1997;
                                                                                                                                                                                                                                                                           Inidentified
                                                                                                                                                                                                                                                                                                                                                         04-MAR-2004.
                                                                                                                    20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blecha F,
                                                                             ADL67258;
RESULT 4
                      ADL67258
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Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

Disclosure; Page 27; 45pp; English

UNIV ) UNIV KANSAS STATE RES FOUND.

WPI; 1996-476842/47. Blecha F, Shi J;

96WO-US004674.

10-APR-1996; 10-APR-1995;

WO9632129-A1

Synthetic.

17-0CT-1996.

95US-00419066.

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AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. The method of the invention. The method comprises administering leukocyte superoxide anion (02-) production. The method comprises administering leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte or production. The peptides can be used as medicaments for fighting dissued amage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 2; Length 23; 100.0%; Pred. No. 0.00023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE86114 standard; peptide; 23 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease states
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Query Match
Best Local Similarity luv...
Best Local 16; Conservative
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Gaps . 0

0; Indels

Mismatches

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RPRPPPFFPPRLPPRI 16 1 RPRPPFFPPRLPPRI 16

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The present invention relates to a method of inhibiting leukocyte superoxide anion (02-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                              Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs
                                                         leukocyte attraction; proline-arginine-rich antimicrobial peptide
PR-rich antimicrobial peptide; neutrophil; wound site; infection;
tissue damage; oxygen radical; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 96; DB 8; Length 23; 100.0%; Pred. No. 0.00023; ive 0; Mismatches 0; IndelB
             Proline-arginine (PR)-rich antimicrobial peptide PR-23
                                              production;
                                            Leukocyte superoxide anion; leukocyte 02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptide PR-39 analog PR-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 3; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL67256 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                    95US-00419066.
                                                                                                                                                                                                                      07-DEC-2001; 2001US-00014147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-059188/06
                                                                                                                                                                                                                                                                                                  (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Blecha F, Shi J;
                                                                                                                                                       US2003125249-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004043934-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             the location.
                                                                                                                                                                                                                                                      10-APR-1995;
08-OCT-1997;
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                                                                                                                          Synthetic.
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ADL67256
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The invention relates to inhibiting leucocyte superoxide anion (02-)

Continiorabial peptide known as PR-39 and its truncated analogs. The

Continiorabial peptide known as PR-39 and its truncated analogs. The

method comprises contacting leucocytes with the peptide comprising 39 or

26 amino acids, for a time and under conditions effective to inhibit

Co leucocyte superoxide anion production. The peptide inhibits the activity

of NADPH oxidase responsible for anion production, by binding to Src

homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein

co f the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or

porcine leucocyte and the mammalian leucocyte is neutrophil. Another

co porcine leucocyte and the mammalian leucocyte is neutrophil. Another

con acids, where the sum of the proline and arginine residues in the

effective peptide is at least 66 or 74 % of the total number of amino

acids. This peptide inhibits leucocyte 02- production by the effective

con peptide are arginine residues. The method of the invention is useful

con peptide are arginine residues. The method of the invention is useful

con peptide are arginine residues. The method of the invention is useful

con thibiting leucocyte oxygen radical production. The peptides are

consecul as medicaments for fighting infections by attracting leucocytes to

a wound site, yet restrict tissue damage at the wound site caused by

conseculate and paralogue by 23 analog by these leucocytes. The present
                                                                                                                                                                                                                                                                    Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; bMA synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; supercoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
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0
               28-AUG-2003; 2003US-00651147.
                                                                              97US-00930777
                                                            95US-00419066
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPRPPFFPPRLPPRI
                                                                                                                                                                                                                                 WPI; 2004-225728/21.
                                                                                                                                                                                      Blecha F, Shi J;
                                                                                                                          (BLEC/) BLECHA F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 AA;
                                                                                                                                              (SHIJ/) SHI J.
                                                         10-APR-1995;
                                                                                08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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Gaps

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WO9632129-A1

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ADE86113;
                                                                    residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                         AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in the method of the invention. These sequences, and PR39, can be used in the method of the invention. The method comprises administering leukocyte alektocyte a peptide (such as this sequence) capable of inhibiting leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte or production. The peptides can be used as medicaments for fighting infection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                        Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 2; I
100.0%; Pred. No. 0.00026;
tive. 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proline/Arginine rich peptide PR-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                      (UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW75723 standard; peptide; 26 AA.
                                                                                                                                                                                                                    Claim 3; Page 26; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US003207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RPRPPPFPPRLPPRI 26
                                                         95US-00419066
                              96WO-US004674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1998 (first entry)
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                                                                                                                                            WPI; 1996-476842/47.
                                                                                                                   Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
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                               10-APR-1996;
                                                           10-APR-1995;
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   17-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                   Blecha F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW75723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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Sequences AAW75722-W75732 are proline/arginine rich peptides that upon administration into a mammal's bloodstream reduce reperfusion injury (production of reactive oxygen species, neutrophila adherence to endothelium, and extravasation of neutrophils). These peptides have two cendethelium, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXR, where P is a compline residue and X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was contablished by structural and function analysis that a peptide should infally contain 4 or 6 of these motifs, and that inhibitory activity is correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the neutrophil superoxide anion, and also the inhibition of neutrophil superoxide anion, and also the inhibition of neutrophil oxidase to some extent. All of the peptides also inhibit neutrophil contains activity. PR-39 is believed, to be the most potent endogenous down regulator of NADPH oxidase yet discovered, and from the data cordinated in injury induced adhesion and extraction of neutrophils. The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery
                                                                   Reduction of reperfusion injury in temporarily occluded blood vessels by administration of a peptide which is rich in proline or arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte superoxide anion; leukocyte O2- production; leukocyte attraction; proline-arginine-rich antimicrobial peptide; PR-rich antimicrobial peptide; neutrophil; wound site; infection; tissue damage; oxygen radical; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proline-arginine (PR)-rich antimicrobial peptide PR-26.
                                                                                                                                                                                                                                           Claim 3; Page 14-15; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE86113 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-00419066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
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WPI; 1998-495359/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS2003125249-A1.
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08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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The invention relates to inhibiting leucocyte superoxide anion (02-)

production using a naturally occurring proline-arginine (PR)-rich
antimicrobial peptide known as PR-19 and its truncated analogs. The
method comprises contacting leucocytes with the peptide comprising 39 or
26 amino acids, for a time and under conditions effective to inhibit
CC leucocyte superoxide anion production. The peptide inhibite the activity
of NADPH oxidase responsible for anion production, by binding to Src
homology 3 (SH3) domain of p47phox, which is a 47 kba cytosolic protein
CC che phagocytic NADPH oxidase complex. The leucocyte is amammalian or
porcine leucocyte and the mammalian leucocyte is neutrophil. Another
CC method is also disclosed which employs a PR-19 analog that comprise 16
CC method is also disclosed which employs a PR-39 analog that comprise 16
CC acids. This peptide is at least 66 or 74 % of the total number of amino
acids, where the sum of the proline and arginine residues in the
CC binding to p47phox in whole cells, therefore interfering with the binding
CC p47phox to p22phox. At least 14 or 25% of the amino acid residues in
CC the peptide are arginine residues. The method of the invention is useful
CC inhibiting leucocyte oxygen radical production. The peptides are
CC a wound site, yet restrict tissue damage at the wound site caused by
CC excessive oxygen radicals produced by these leucocytes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New anti-bacterial polypeptide - active against Gram negative bacteria
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veterinary medicine; prophylactic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 96; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joernvall H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR30491 standard; peptide; 39 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   excessive oxygen radicals produ
sequence is PR-39 analog PR-26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial peptide
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(BOMA/) BOMAN H G.
(MUTT/) MUTT V.
(JOER/) JOERNVALL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-018080/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 AA;
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12-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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%$GGGGGGGGGGGGGGGGGGG
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                                                                                                                                                                                                                                                                          , or
are
                                                                                                                                                                       The present invention relates to a method of inhibiting leukocyte superoxide anion (O2-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                        Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-26.
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    .3
/note= "Essential for antibacterial activity"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 8; Length 26; 100.0%; Pred. No. 0.00026; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide PR-39 analog PR-26.
                                                                                                                                   Claim 3; SEQ ID NO 2; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2; 24pp; English
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97US-00930777.
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Best Local Similarity 100.
Matches 16; Conservative
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WPI; 2004-059188/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-225728/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blecha F, Shi J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1995;
08-OCT-1997;
                                                                                        the location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jnidentified
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ADL67255
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Gaps ; 0 1 RPRPPPFFPPRLPPRI 16

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AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be used to treat sexually transmitted diseases (STDS) caused by Chlamydia, HIV, herpes simplex virus, Neisseria gomorhoeae or Candida infection. The peptides inhibit STDS by either killing the infectious organism, impeding the infection mechanism or interrupting the replication cycle of the organism. Squalamine (an aminosterol host defence molecule of the dog fish shark Squalus canthias) and PGLa (a frog antimicrobial peptide) analogues may also be useful in inhibiting STD infection and transmission
inestine is an important endocrine organ and many physiologically active peptides have been isolated from it. This peptide inhibits the growth of, and may kill, bacteria, pref. gram negative bacteria. This peptide or its functional derivatives may be used in human or veterinary medicine for therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STD; sexually transmitted disease; HIV; human immunodeficiency virus; herpes simplex virus; HSV; Neisseria gonnorhoeae; Candida; Chlamydia; magainin; antimicrobial; squalamine.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting sexually transmitted disease e.g. HIV or herpes simplex administering magainin antimicrobial or squalamine cpd. to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                   Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 100.0%; Score 96; DB 2; Length 39; Local Similarity 100.0%; Pred. No. 0.00037; No. 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  100.0%; Score 96; DB 2; Length 39; 100.0%; Pred. No. 0.00037; Eive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bedi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 32; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams T,
                                                                                                                                                                                                                                                                                                                                    AAR99121 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US011675
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                                                                                                                                                                                                                     1 RPRPPFFPPRLPPRI 16
                                                                                                                                                                                                                                           RPRPPPFFPPRLPPRI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAGA-) MAGAININ PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zasloff M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-179725/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39 AA;
                                                                                                                        Sequence 39 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9608270-A2
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Best Local S:
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                       AAR99121;
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                                                                                                                                                                                                                                                                                                       RESULT 13
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The present peptide is a synducin, which induces the expression of syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp. fibroblasts and epithelial cells. The 36 N-terminal amino acids of the opeptide were found to be identical to the 36 N-terminal amino acids of PR-98 peptide were found to be identical to the 36 N-terminal amino acids of Resistances in the proposed previously found in porcine intestine (W09222578). Synducins may be used in the treatment of stasis and decubitus ulcers, keloids, skin burns, ischemic tissues and hypercoagulation states, prevention of tumour metastasis, restenosis inhibition and endothelial cells were assayed for syndecan-4 expression following exposure to 5 % wound fluid, dbcAMP (1 mM), the present peptide (10 microM) or a blank, to give respective cell surface syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating mesenchymal interaction by administration of synducin - used in the treatment of wounds, tumours, restenosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                            Synducin; induction; expression; syndecan-1; syndecan-4; surface; mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis; decubitus; ulcers; keloids; skin burns; ischemic tissues; hypercoagulation states; prevention; tumour metastasis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                inhibition; angiogenesis; proliferation; endothelial
                                                                                                                                                                                              Synducin peptide (PR-39) induces syndecan expression
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100.0%; Pred. No. 0.00037;
tive 0; Mismatches 0;
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                                                                                             AAR94446 standard; peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 26; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00310722.
                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US012080.
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1 RPRPPPFFPPRLPPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIL-) CHILDRENS MEDICAL
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                                                                                                                                                                05-NOV-1996 (first entry)
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallo RL, Bernfield M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-188401/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                     WO9609322-A2
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                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                AAR9446;
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AAW01446
                                                                 RESULT 14
                                                                                  AAR94446
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This sequence represents the proline-arginine rich antimicrobial peptide PR39. The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenthymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well of a in antibacterial agents. This sequence, and the fragments of it shown in AAW01447-W01454, can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (02-02) production. The method contine the method of the invention is for inhibiting leukocyte of peptide (such as this sequence) capable of inhibiting leukocyte of peptide. The peptides can be used as medicaments for fighting infection by attracting leukocytes, to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating inflammatory disease states
                                                                             Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; DNA syntheals; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
                                       Leukocyte O2- production inhibitor peptide PR39
                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 26; 45pp; English.
                                                                                                                                                                                                                                                                                                                                              96WO-US004674
                                                                                                                                                                                                                                                                                                                                                                                      95US-00419066
  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 AA;
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                                                                                                                                                                                                                                                                                                                                              10-APR-1996;
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18-JUN-1997
                                                                                                                                                                                                                                                                                                    17-0CT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blecha F,
                                                                                                                                                                                                                Synthetic
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Query Match 100.0%; Score 96; DB 2; Length 39; Best Local Similarity 100.0%; Pred. No. 0.00037; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

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8 8

Search completed: October 26, 2005, 05:12:07 Job time : 65.9818 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 26, 2005, 05:00:14; Search time 11.9273 Seconds (without alignments) 129.071 Million cell updates/sec

US-10-014-147-5 96 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RPRPPFFPPRLPPRI 16 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	antimicrobial prot	=		hypothetical prote	like	14	hypothetical prote	dishevelled homolo	ы			_	fibrillin-1 precur		troponin T, cardia	rece	E-Ì	Ļ	H	troponin T cardiac			hypothetical prote		pept	rich pr		u	nucleic acid-bindi
ΩI	868232	JQ1663	T24158	T24157	S57330	S40463	A33507	121691	T30351	T26608	C69432	T26998	A55624	T48490	TPCHTC	B47417	B25345	A25345	A28008	I46903	T45564	T00074	D84672	S10782	PJHUSB	JC5572	S14981	S34163	JC4525
jth DB	172 2		2584 2		212 2		•	736 2	2 620	164 2	٠.	•	871 2	213 2	302 1	540 2	276 2	276 2	284 2			903 2	134 2	57 2		134 2			305 2
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Result No.	-	7	e	4	2	9	7	œ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

cytokinin-induced RNA/DNA-binding pr	proline-rich prote homeotic protein H	homeotic protein H protein-tyrosine k	probable nuclear a	hypothetical prote	spore coat protein	infected cell prot	hypothetical prote	fas ligand - rat	cell wall protein	proline-rich prote	extensin - Volvox	F44B9.3 protein -
T10064 S43417	S27200 S34164	S47539 T18276	B45344	B40505	A41051	JQ1682	T00080	A49266	S52985	T51407	S22697	S44814
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329 365	389 411	417	1733	1958	82	248	1560	278	381	401	464	544
54.2 54.2	54.2	54.2	54.2	54.2	53.6	53.6	53.6	53.1	53.1	53.1	53.1	53.1
52 52	5 5 7 7 7 7	52	25	52	51.5	51.5	51.5	51	51	51	51	51
30 31	3 B	3.4	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 S66232 antimicrobial protein NyAtternate names: m C;Species: Sus scrof. C;Date: 15-Feb-1997 C;Accession: S68232; R;Zhao, C; Garz, T: FEBS Lett. 376, 130- A;Ritle: Structures A;Reterne unuber: A;Residues: 1-172 <2 A;Residues: 1-20,'A' A;Residues: 1-20,'	S68232 antimicrobial protein PR-39 precursor, cathelin-associated - pig N;Alternate names: myeloid antibacterial protein PR-39 C;Species: Sus scrofa domestica (domestic pig) C;Date: 15-Peb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004	C,Accession: S68232; JN0899; 141138; S19563 R;Zhao, C.; Ganz, T.; Lehrer, R.I. FEBS Lett. 376, 130-134, 1995 A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni A;Tetle: Structures of A;Tetle: Structures of A;Tetle: Structures of A;Tetle: A;Tetle: Structures of A;Tetle: Status: translation not shown A;Status: translation not shown A;Molecule troe: DNA	A;Residues: 1-172 <zha> A;Residues: 1-172 <zha> A;Residues: 1-172 <zha> A;Cross-references: UNIPROT: P80054; EMBL: X89201; NID: g1165150; PIDN: CAA61487.1; PID: g1165 A;Cross-references: Universe: leukocytes A;Experimental source: leukocytes B;Storici, P.; Zanetti, M. Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993 Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993 A;Title: A CDNA derived from pig bone marrow cells predicts a sequence identical to the 3 A;Reference number: JN0899; MUID: 94071853; PMID: 8250863 A;Accession: JN0899</zha></zha></zha>	A; Molecule Cype: mixwa. A; Molecule Cype: mixwa. A; Residues: 1-20, A', 22-172 <sto> A; Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101 A; Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101 A; Experimental source: Done marrow cells B; Cudmundsson, G. H.; Magnusson, K. P.; Chowdhary, B. P.; Johansson, M.; Andersson, L.; Bome A; Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami A; Reference number: 147138 A; Accession: 147138 A; Accession: 147138 A; Molecule type: DNA /sto>	A;Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298 R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall, A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of the A;Reference number: S19563; MUID:92111534; PMID:1765098 A;Accession: S19563 A;Molecule type: protein A;Residues: 131-169 <age> A;Experimental source: intestine C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Antrons: 66/3; 102/3; 126/3</age>	C,Superfamily: cathelin; cystatin homology K;Keywords: amidated carboxyl end; antibacterial F;1-29/Domain: signal sequence #status predicted <sig> F;22-129/Domain: cystatin homology <cys> F;30-139/Domain: propeptide #status predicted <pro> F;30-130/Domain: antimicrohial profein PR-39 #status experimental <wat></wat></pro></cys></sig>
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C; Accession: S57330; S68726
R; Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V. Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A; Title: Molecular cloning and identification of a novel porcine cathelin-like antibacter A; Reference number: S57330; MUID: 96042752; PMID: 7576250
                                                                                                                                                                                                                                                      R;Bardill, S.
submitted to the EMBL Data Library, April 1996
A;Recession: T24157
A;Accession: T24157
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-2606 < WILL>
A;Residues: 1-2606 < WILL>
A;Cross-references: UNIPROT:Q21920; EMBL:Z70686; PIDN:CAA94615.1; GSPDB:GN00022; CESP:R11
A;Experimental source: clone R10H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 24/3; 80/3; 137/2; 177/1; 218/3; 348/3; 507/2; 709/3; 753/2; 924/1; 1020/3; 10
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A;Residues: 1-212 <STR>
A;Residues: 1-212 <STR>
A;Residues: 1-212 <STR>
A;Cross-references: UNIPROT:P51524; GB:X86031; NID:g1006756; PIDN:CAA60023.1; PID:g100675
R;Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I.
FEBS Lett. 362, 65-69, 1995
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A,Reference number: S68726; MUID:95212585; PMID:7698355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:270310; PIDN:CAA94370.1; GSPDB:GN00022; CESP:R11A8.7a
A;Experimental source: clone R11A8
                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24157; T24177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment) N,Alternate names: antimicrobial peptide; prophenin-1 C;Species: Sus scrofa domestica (domestic pig) C;Date: 27-C61-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%; Score 59; DB 2; Length 2606; 64.3%; Pred. No. 25;
                                                                                                                         hypothetical protein R11A8.7a - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cummings, P. submings, P. submings, P. submitted to the EMBL Data Library, March 1996 A;Reference number: Z19849 A;Accession: T24177
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A,Residues: 131-209 «HAR»
A,Experimental source: laukocytes
C,Superfamily: cathelin; cystatin homology
C,Keywords: antibacterial
F,6-113/Domain: cystatin homology <CYS»
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Matches 9, Conservative
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A; Residues: 1-2606 <WI2>
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F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl
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A;Residues: 1-301 <1058
A;Cross-treferences: UNIPROT:Q41848; EMBL:X60432; NID:g433706; PIDN:CAA42959.1; PID:g4337
A;Experimental source: strain W64A
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2584 «WIL»
A;Cross-references: UNIPROT:Q9TW88; EMBL:Z70686; PIDN:CAB54289.1; GSPDB:GN00022; CESP:R1
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A;Introns: 24/3; 80/3; 137/2; 177/1; 218/3; 348/3; 507/2; 709/3; 753/2; 924/1; 1020/3;
                                                                                                                                                                                                                                                                                                                                                                                                                  hybrid proline-rich protein - maize
hybrid proline-rich protein - maize
C;Species: Zea mays (maize)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: J01663
R;Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
Plant Cell 4, 413-423, 1992
A;Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein. A;Reference number: J01663; MuID:92361259; PMID:1498600
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A;Reference number: 219849
A;Reference number: 219849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2584 < WIZ>
A;Cross_references: EMBL: Z70310; PIDN:CAB54294.1; GSPDB:GN00022; CESP:R11A8.7b
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                         100.0%; Score 96; DB 2; Length 172; 100.0%; Pred. No. 6.6e-05; Live 0; Mismatches 0; Indels
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R;Bardill, S.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z19846
A;Accession: T24158
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                                                                                                                                                                                                                                                          141 KPRPPPFPPKLPPKI 156
                                                                                                                                                                                                1 RPRPPPFFPPRLPPRI 16
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179 RPSPPPYVPPYVPP 192
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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Indels

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Gaps .. 0

3 RPPPFFPPRLPPR 15

8

2499 RPQPPPVAPQAPP 2512

Length 212; Indels 64 PAPPAPAFPPQLPPHV 79

셤

199 RPPPFGPPRFPGR 211

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A; Molecule type: mRNA A; Residues: 1-228 <PUN>

A; Status: preliminary A; Accession: S40463

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C;Accession: T30351
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrn
Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d3
A;Reference number: Z20836; MUID:99124785; PMID:9887315
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A;Residues: 1-164 <WIL>
A;Cross-references: UNIPROT:Q9XXG3; EMBL:AL023835; PIDN:CAA19486.1; GSPDB:GN00022; CESP:)
A;Experimental source: clone Y37A1B
                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-736 <SOK>
A;Cross-references: UNIPROT:P51142; EMBL:U31552; NID:9945109; PIDN:AAB00688.1; PID:994511
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C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                       disfievelled homolog - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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A;Cross-references: UNIPROT:Q9YMX0; EMBL:AF081810; PIDN:AAC70189.1
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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57.8%; Score 55.5; D

Best Local Similarity 52.4%; Pred. No. 25;

Matches 11; Conservative 1; Mismatches
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F;260-336/Domain: GLGF domain homology <GLG4>
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98 RPEPPPVPPIPP 111
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Best Local Similarity 64.3.
Local Similarity 64.3.
Local Similarity 64.3.
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
C;Accession: A33507
C;Accession: A33507
D; Biol: Chem. 264, 10057-10064, 1989
A;Futile: Isolation and characterization of CDNA clones derived from the divergently tran A;Reference number: A33507; MUID:89255490; PMID:2722860
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                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P51525; EMBL:X75438; NID:g443812; PIDN:CAA53188.1; PID:g4438
R;Strukelj, B.; Pungercar J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V
Biol. Chem. Hoppe-Seyler 376; SOF-510, 1995
A;Itle: Monecular cloning and identification of a novel porcine cathelin-like antibacte
A;Reference number: S57330; MUID:96042752; PMID:7576250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S57331
A;Status: preliminary
A;Molecule type: mRNA
A;Medlecule type: mRNA
A;Medlecule : 1-228 <STR>
B;Zhao, C.; Ganz, T.; Lehrer, R.I.
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
A;ResS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen A;Reference number: 868232; MUID:96105365; PMID:7498526
prophenin (PF-2) precursor - pig
NiAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40463; S57331; $68233
K;Pungercar, J; Strukelj, B; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk,
FEBS Lett. 336, 284-288, 1993
A;Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
A;Reference number: S40463; MUID:94085623; PMID:8262247
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A;Residues: 1-228 <ZHA>
A;Cross-references: EMBL:X89202; NID:g1165148; PIDN:CAA61488.1; PID:g1165149
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Query Match 60.4%; Score 58; DB 2; Length 228; Best Local Similarity 76.9%; Pred. No. 2.9; Matches 10; Conservative 0; Mismatches 3; Indels

215 RPPPFGPPRFPGR 227

g 8

A33507

3 RPPFFFPRLPPR 15

A;Introns: 66/3; 102/3; 126/3 C;Superfamily: cathelin; cystatin homology T;1-29/Domain: signal sequence #status predicted <SIG> F;22-129/Domain: cystatin homology <CYS> F;30-228/Product: prophenin (PF-2) #status predicted <MAT>

Status: preliminary

Accession: S68233

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ä
19.9%; Score 56.5; DB 2; Length 1137; ilarity 62.5%; Pred. No. 21; Conservative 2; Mismatches 3; Indels 1.
                              Best Local Similarity
Matches 10; Conserv
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A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1137 <FUJ>

Query Match

A; Accession: A33507 A; Status: preliminary

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Rivin, W.; Smiley, E.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, L.; Ramirez, F. J. Biol. Chem. 270, 1798-1806, 1995
A.fitele: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ger A; Reference number: A55624; MUID:95130561; PMID:7829516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryo-specific protein 3 (ATS3) - Arabidopsis thaliana
AlAlternate names: protein T2814.130
C;Alternate names: protein T2814.130
C;Alternate names: protein T2849.
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48490
R;Bevan, M: Murphy, G; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lengubmitted to the Protein Sequence Database, April 2000
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J. Biol. Chem. 260, 11140-11148, 1985
A;Title: A single cardiac troponin T gene generates embryonic and adult isoforms via deve
A;Reference number: A25373; MUID:85289327; PMID:2993302
                                                                                                                                                                                    A;Accession: A55624
A;Status: preliminary
A;Molecule type: mRNA
A;Rolecules: 1-2871 <YIN>
A;Cross-references: UNIPROT:Q61554; GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1.302 <CCO>
A;Cross-treferences: UNIPROT:P02642; GB:M10013; NID:g212783; PIDN:AAA49099.1; PID:g212784
R;Cooper, T.A.; Ordahl, C.P.
Science 226, 979-982, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-213 <BEV>
A;Cross-references: UNIPROT:Q9LYP6; EMBL:AL163652
A;Experimental source: cultivar Columbia; BAC clone T28J14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 2, Pred. No. 8.1; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.3%; Score 55; 58.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                     A;Gene: Fbn-1
C;Superfamily: fibrillin; EGF homology
F;1201-1236/Domain: EGF homology <EGF>
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0
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 5
A;Introns: 28/3; 65
A;Note: T28J14.130
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69432
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
Fleistchmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: 220297
A;Accession: T26998
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosesidues: 1-716 <WILL>
A;Cross-references: UNIPROT: Q9U2A6; EMBL: AL110490; NID: e1542263; PIDN: CAB54442.1; CESP: X
A;Experimental source: clone Y48B6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:028812; GB:AE001002; GB:AE000782; NID:g2689325; PIDN:AAB8979
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C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C'Accession: T26998
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                                                                                             Score 55; DB 2; Length 164;
Pred. No. 4.8;
0; Mismatches 3; Indels
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A;Introns: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lypothetical protein Y48B6A.6 - Caenorhabditis elegans
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69.2%; Pred. No. 20;
tive 1; Mismatches
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                                                                                                        57.3%;
75.0%;
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fibrillin-1 precursor - mouse
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Best Local Similarity '
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Best Local Similarity
Matches 9; Conserva
                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
  A,Gene: CESP:Y37A1B.2a
                      A; Map position: 4
A;Introns: 32/3; 66/3
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A;Gene: CESP:Y48B6A.
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A;Title: A single troponin T gene regulated by different programs in cardiac and skeleta A;Reference number: A03086; MUID:85065747; PMID:6095446
A;Accession: A03086
A;Accession: A03086
A;Accession: A03086
A;Accession: A03086
A;Coos-references: GB:702263; MID:9212781; PIDN:AAA49098.1; PID:9212782
C;Comment: This protein, found in adult cardiac muscle and transiently in embryonic skel and skeletal muscle. Down-regulation of the protein in the late stages of skeletal muscl C;Superfamily: troponin T
C;Keywords alternative splicing; cardiac muscle; differentiation; heart; muscle; phosph F;1.302/Product: troponin T, cardiac muscle, embryonic splice form #status predicted <MA F;1-22,33-302/Product: troponin T, cardiac muscle, adult splice form #status predicted <
```

0; Gaps

Query Match
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 4; Mismatches 4; Indels

Search completed: October 26, 2005, 05:19:59 Job time: 12.9273 secs

1 RPRPPFFPPRLPPRI 16 :|:||||:||:| 78 KPKPKPFMPNLVPPKI 93

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This Page Siank (uspic)

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

October 26, 2005, 04:52:03; Search time 55.4182 Seconds (without alignments) 147.844 Million cell updates/sec

US-10-014-147-5 score: Title: Perfect :

1 RPRPPFFPPRLPPRI 16 **BLOSUM62** Scoring table: Sequence:

1612378 segs, 512079187 residues Searched:

Gapop 10.0 , Gapext 0.5

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries UniProt 03:\*

1: uniprot\_sprot:\* 2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sus		human pap		O7pqg9 anopheles g	homo homo	homo	mus		homo	mus	พนธ น	homo	рошо			-	caenor	oryza	oryza	oryza	oryz	P51524 sus scrofa			Occahs kluyveromyc	arabid	oryza	oryza	esk7 oryza s	Q8s9b5 volvox cart
SUMMARIES	ID	PR39 PIG	FBSH MOUSE	Q99FW9	Q41848	Q7PQG9	Q96F80	QBWVN3	041660	Q8BWX7	О9Н077	Q9DBB2	Q9D824	Q6UN15	DTX3 HUMAN	DTX3 MOUSE	Q7SC01	Q9TW88	Q21920	QGETT6	О6Н843	Q67VV4	Q6Z4P0	PF11_PIG	PF12_PIG	Q63Z <u>L</u> 7	ОССОН5	Q9FG86	Q6Z8Z0	Q9XIZ3	Q6ESK7	Q8S9B5
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	* Query Match Length	172	378	103	301	2133	328	378	208	513	520	545	581	594	347	347	1395	2584	2606	105	139	150	150	212	228	586	908	187	228	333	548	.625
	% Query Match	100.0	65.6	63.5	63.5	63.5	62.5	62.5	62.5			62.5	62.5	62.5	61.5	61.5	61.5	61.5	61.5	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	59.4	თ	59.4	σ	59.4
	Score	96	63	61	61	61	9	9	9	9	9	9	9	9	59	59	59	59	59	58	58	58	28	58	58	58	58	57	57	57	57	57
	Result No.		7	е	4	Ŋ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		59		

Q789h3 neurospora P20585 homo sapien Q86ug6 homo sapien Q62186 cryza sativ Q7xii7 cryza sativ Q9han7 homo sapien Q811Q0 plasmodium Q6ntp8 xenopus lae	P51142 xenopus lae Q9ymxO lymantria d Q9xxg3 caenorhabdi Q9fi79 arabidopsis O28812 archaeoglob
Q789H3 Q7RYV7 MSH3 HUMAN Q66UG6 Q62L86 Q7XI17 FBSH HUMAN Q81LQ0 Q6NTP8	DVL2_XENLA Q9YNK0 Q9XNG3 Q9X179 YE60_ARÇFU
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825 1137 1140 165 196 372 488	736 1029 164 205 227
4 0 0 0 0 0 0 0 0	m & m m m
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	55 55 55 55 55 55
######################################	44444 122844 2433

# ALIGNMENTS

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TISSUE=Neutrophils;
MEDININE=95088504; Pubmed=7996056;
Shi J., Ross C.R., Chengappa M.M., Blecha F.;
"Identification of a proline-arginine-rich antibacterial peptide from
                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=95350216; PubMed=7624374;
Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
Andersson L., Boman H.G.;
"Structure of the gene for porcine peptide antibiotic PR-39, a
cathelin gene family member: comparative mapping of the locus for the
human peptide antibiotic FALL-39.";
Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Intestine;
MEDLINE=92111534; PubMed=1765038;
Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
Mutt V., Joernvall H.;
"Amino acid sequence of PR-39. Isolation from pig intestine of a new
member of the family of proline-arginine-rich antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=5610, 505365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3; Zhao C., Ganz T., Lehrer R.I.; "Structures of genes for two cathelin-associated antimicrobial peppides: prophenin-2 and PR-39.";
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bone marrow;
MEDLINE=94071853; PubMed=8250863;
Storici P., Zanetti M.;
"A cDNA derived from pig bone marrow cells predicts a sequence identical to the intestinal antibacterial peptide PR-39.";
Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
                            PR39 PIG STANDARD; PKI; 1,2 cn. 180054; OGTR84; Corrected) 01-0CT-1996 (Rel. 21, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Antibacterial protein PR-39 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 202:849-854(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 131-164, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 376:130-134(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 131-169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                       Sus scrofa (Pig).
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              PR39_PIG
RESULT 1
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N

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TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=2354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
neutrophils that is analogous to PR-39, an antibacterial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                     the small intestine.";
J. Leukoc. Biol. 56:807-811(1994).
-!-FUNCTION: Exerts a potent antimicrobial activity against both E.coli and B.megaterium.
-!- TISSUE SPECIFICITY: Small intestine and bone marrow.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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By similarity.
Proline amide (G-170 provides amide
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Pyrrolidone carboxylic acid (By
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994B792798C0E133 CRC64;
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G -> A (in Ref. 1).

A -> T (in Ref. 1).

RQ -> QR (in Ref. 1).

IHS -> NDP (in Ref. 1).

P -> I (in Ref. 5).
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EMBL; K88201; CAA64487.1; --
PIR; S68232; S68232.
HSSP; P32196; 1KWI.
InterPro; IPR001894; Cathelicidin.
ProDom; P0001898; Cathelicidins; 1.
PROSITE; PS00947; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Amidation; Antibiotic; Direct protein sequencing;
Pyrrolidone carboxylic acid; Signal.
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25-00T-2004 (Rel. 45, Last sequence update)
25-00T-2004 (Rel. 45, Last annotation update)
Probable fibrosin 1 long transcript protein.
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117 1
157 1
172 AA;
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Length 378;

Score 63; DB 1; Pred. No. 11;

65.6%;

Query Match Best Local Similarity

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1941 RPPSYYPPRLPP 1952
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"Complete nucleotide sequence and analysis of a novel human
papillomavirus (HPW 84) genome cloned by an overlapping PCR method.";
virology 279:109-115(2001).
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MEDINE=29159; PubMed=1498600;
MOSTHNE=291501
MOSTHE Avila L., Puigdomenech P.;
"A maize embryo-specific gene encodes a proline-rich and hydrophobic
                                                                                                                                                                                                                                                                                                                                                              Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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MEDLINE=21066735; PubMed=11145894; DOI=10.1006/viro.2000.0716;
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                                                                                                                                                                                                                                                                                                                                       63.5%; Score 61; DB 2; Length 103; 73.3%; Pred. No. 5.1; 1; ve. 0; Mismatches 4; Indels
Indels
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EMBL; X60422; CAA42959.1; --
ENF, JQ1663; JQ163..
HSSP; P24337; 1HYP.
InterPro; IPR003612; AMI.
PFfam; PF00224; Tryp_alpha_amyl; 1.
SMART; SM00493, AMI; 1.
SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;
                                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Putative B4 procein.
Human papillomavirus type 84.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                   EMBL, AF293960; AAK09275.1; -.
InterPro; IPR003861; Papilloma_E4.
Pfam; PF02711; Pap_E4; 1.
SEQUENCE 103 AA; 11162 MW; 2C32F1FD23337E55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                   (TrEMBLrel. 17, Created)
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Mismatches
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                                         259 RPRPPFLGPSLPER 273
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                                                                                                                                                                                     Papillomavirus.
NCBI_TaxID=150546;
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01-JUN-2001
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DE CANARAZONA (TERRELEA) 26, Lest sequence update)

DE CANARAZONA (TERRELEA) 26, Lest sequence update)

DE CANARAZONA (TERRELEA) 26, Lest sequence update)

ON CANARAZONA (TERRELEA) 26, Lest sequence update)

NAMMS=REANNEDOGONO17221 (Fragment)

NAMMS=REANNEDOGONO17221 (Fragment)

NAMMS=REANNEDOGONO17221 (Fragment)

RA ALORDELS GEORGE SEQUENCE DISPLETA NEMBERCEA; PLETYQUCA;

NAMMS=REANNEDOGONO17221 (Fragment)

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                                                                                                                    Fipll1 protein.
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                               Q99LH0;
Q99LH0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   62.5%; Score 60; DB 2; Length 328; 75.0%; Pred. No. 21;
                                                                                                                                                                                                     2; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017724; AAH17724.1; -.
Pfam; PF05182; Fipl; 1.
SEQUENCE 378 AA; 40834 MW; 1B699B114C9560D4 CRC64;
                                                                 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011543; AM11543.1; -.
NON TER
                                                                                                                                SEQUENCE 328 AA; 37615 MW; 38472A76B3E8A1B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                  Query Match
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Best Local 9; Conservative
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89 KPPPFFPPGAPP 100
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NCBI_TaxID=9606;
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STRAIN=FVB/N; TISSUE-Mammary tumor. C3;

MEDINNE-2238825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhata N.K.,

A Dischal R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

A Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brossk S.A., McEwan P.J., McKernan R.J., Malk J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley N., Sodergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
enriched library, clone:C530020P17 product:weakly similar to TOMATO
CELL WALL HRGP (HYDROXPROLINE-RICH GLYCOPROTEIN) (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodenția; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003263; AAH03263.1; -
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InterPro; IRR007854; Fipl.
PHEM: PF05182; Fipl; 1.
SEQUENCE 508 AA; 55796 MW; 01BF436596282ED4 CRC64;
                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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508 AA.
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                           Created)
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                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
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PRELIMINARY;
                                                                                                                                                                                                                                       Name=Fip111;
Mus musculus (Mouse)
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Q9DBB2
                                                                                                            Q9H077
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Q9DBB2
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A dachi J. Aizawa K. Akimura T., Arakawa T., Bono H., Carninci P.,
A dachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Puruno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiranoto K., Hiraoka T., Hirozane T.,
A Katch H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saito H., Sakai C., Sakai K., Sakazume N., Sano H.,
A sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yaguni M., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subbraction of cap-trapper-selected cDNAs to prepare fiuli-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
SEQUENCE FROM N.A.
STRAIN=CS7BL/60; TISSUE=Spinal cord;
MEDLINE=99279213; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
CARTHOR P., HAYABHIZARI Y.;
"High-efficiency full-length cDNA cloning.";
Migh-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/61; TISSUB=Spinal cord; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Pujiwake S., Inoue K., Togawa M., Ohara B., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
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STRAIN-C57BL/6J; TISSUE-Spinal cord;
The FANTOM Consortium,
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                 RIKEN FANTOM Consortium;
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STRAIN=C57BL/6J; IISSUE-Liver;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UIN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone.1300019H17 product:weakly similar to TOMATO CELL WALL
HRGP (HYDROXPROLINE-RICH GLYCOPROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60; DB 2; Length 520;
Pred. No. 33;
1; Mismatches 2; Indels
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STRAINESSYBL/6J; TISSUE=Liver;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMBOILLUM;
                                                                                                                                                                                                                                                                                                            Fobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                              520 AA; 58375 MW; 55D48285A046A783 CRC64;
                                                      Last sequence update)
Last annotation update)
520 AA
                                      Created)
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                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sec
01-UNN-2003 (TrEMBLrel. 24, Last ant
Hypothetical protein DKF2p586K0717.
Name=DKF2p586K0717;
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75.0%;
                                                                                                                                                                                                                                                                      The German cDNA Consortium;
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281 KPPPFFPPGAPP 292
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  PRELIMINARY;
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                                                                                                                                                                                                                                                        FISSUE=Uterus;
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01-JUN-2001
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2; Indels

1; Mismatches

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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Pukuda S., Fukunishi Y., Puruno M.,
A rakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Puruno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hato H.,
A motani X., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
Muramateu M., Hayashizaki Y.;
EMBL, AKOOSOGI: BAB23785.1; --
                                                                                         SEQUENCE FROM N.A.
SEQUENCE STBL.
STRAIN=C57BL/G17 IISSUE=Liver;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibara K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishih K., Hazama M., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishika J., Ishikawa T., Sakaguchi S., Kira A., Hayashizaki Y.; Rishika J., Ishika J., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult male small intestine cDNA, RIKEN full-length
enriched library, clone:2010310H32 product:weakly similar to TOM
CELL WALL HRGP (HYDROXPROLINE-RICH GLYCOPROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 AA; 61059 MW; D8C65A7E20CA0985 CRC64;
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
      60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR007854; Fipl.
                                   Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||||||||
295 KPPFFPPGAPP 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1914149; Fip111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RPPPFFPPRLPP 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF05182, Fipl,
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                          [5]
SEQUENCE
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Matches
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Q9D824
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Arakawa T., Boro H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Hara A., Hayatsu N., Hiramcto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Fijima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

EMBL, AKOO8551, BAB25745.1; --

EMBL, AKOO8551, BAB25745.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRANT-ESTBL/GJT IISSUE-Small intestine;
STRANT-ESTBL/GJT IISSUE-Small intestine;
The FANTOW CONSORtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Small intestine;
MEDLINE=20499314; PubMed=11042159; DOZI=10.1101/gr.145100;
MEDLINE=20499314; PubMed=11042159; DOZI=10.1101/gr.145100;
MEDLINE P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRIN=CS7BL/6J; TISSUE-Small intestine;
STRIN=CS7BL/6J; TISSUE-Small intestine;
STRIN=CS7BL/6J; TISSUE-Small intestine;
Shibata K., Itoh M., Airawa K., Nagaoka S., Sasaki N., Carrinci P., A MEDLINE-20530913; PubMed-11076861; DOIL S., Sasaki N., Carrinci P., A MEDALA K., Itoh M., Airawa K., Nagaoka S., Hazama T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., A vamamoto R., Inoue K., Toawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y., A Okazaki Y., Muramateu G., Riska M., Hayashizaki Y., Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                 [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 7820, 601, 1188UE-Small intestine;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMSORTIUM;
RIKEN FANTOM COMSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 60; DB 2; 75.0%; Pred. No. 37;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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1; Mismatches
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Pfam; PF05182; Fipl; 1.
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331 KPPPFFPPGAPP 342
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Matches 9; Conservative
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TISSUB-CEREBELLUM, and Teratocarcinoma;

You car T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A car T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Yamanoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

B shiratoria A., Sudo H., Hosoiri T., Kaku Y., Kodatara H., Kondo H.,

A shiratoria A., Sudo H., Hosoiri T., Yamania H., Warakawa M.,

B sugawara M., Takahashi M., Katsuta N., Sato K., Tanikawa M.,

A mazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

Rujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

Rusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

Numura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

Numura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

Namashino K., Yuuki H., Oshima A., Sano S.,

Nomiyama H., Satoh N., Takani S., Teraenshima Y., Suzuki O.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Namadaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami T.,

Namadaki H., Watanabe T., Sugiyama A., Takemoto M., Pujiwara T.,

Namadaki M., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

Rujimori Y., Komiyama H., Zaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

Kawabata A., Hikiji T., Koguteke N., Inagaki H., Ikema Y., Okamoto S.,

Kawabata A., Hikiji T., Koguchi S., Itoh T., Shigeta K., Senba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                         SECURETORIES, STATEMENT, STATEMENT, STATEMENT, STATEMENT, STATEMENT, DOI=10.1038/sj.emboj.7600070; PubMed=14749727; DOI=10.1038/sj.emboj.7600070; Raufmann I., Martin G., Friedlein A., Langen H., Keller W.; Kaufmann I., Martin G., Friedlein A., Langen H., Keller W.; Human Fipl is a subunnit of CPSF that binds to U-rich RNA elements and stimulates poly(A) polymerase."; EMBD. 3736510; AAQ88277.1; -. InterPro; IPR007854; Fipl.
Pfam; PP05182; Fipl.
Pfam; PP05182; Fipl. 1. SEQUENCE 594 AA; 66526 MW; B391D142419ED061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 60; DB 2; Length 594; 75.0%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                               05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Pre-mRNA 3'end processing factor FIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTX3 HUMAN STANDARD; PRT; 347 AA. QBN9I9; QBNDI8; QBNDS8; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2005 (Rel. 46, Last amoutation update) Deltex protein 3 (Deltex-3) (Deltex3).
                 594 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). TISSUE-Cerebellum, and Teratocarcinoma;
                                  Q6UN15;
05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 KPPPFPPGAPP 366
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RPPPFFPPRLPP 14
                 PRELIMINARY;
                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=9606;
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   Q6UN15
ID Q6UN15
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MEDLINE-22679154; PubMed=12670957; DOI=10.1074/jbc.M301157200;
A Takeyama K., Aquiar R.C.T., Gu L., He C., Freeman G.J., Kutok J.L.,
Aster J.C., Shipp M.A.;
A ster J.C., Shipp M.A.;
The BAL-binding protein BBAP and related Deltex family members
arrholt ubsquitin-protein isopeptide ligase activity.";
J. Biol. Chem. 278:1230-21937(2003).
C.I. FUNCTION: Regulator of Notch signaling pathway
involved in cell-cell communications that regulates a broad
spectrum of cell-fate determinations. Probably acts both as a
positive and negative regulator of Notch, depending on the
developmental and cell context (By similarity). Functions as an
developmental and cell context (By similarity). Functions as an
ubiquitin ligase protein in vitro, suggesting that it may regulate
the Notch pathway via some ubiquitin ligase activity.
C. I- SUBUNIT: Homomultimer. May form a heteromultimer with other
members of the Deltex family. Interacts with NOTCH1 (By This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ö Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Makabima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura Y., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human TISSUE=Brain; Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. Gaps Alternative splicing, Metal-binding, Notch signaling pathway; Zinc; RING-type.
Pro-tich.
MSFVLSR -> MPILSSSGSK (in isoform 2)
/FTId=VSP\_008354. ö Score 59; DB 1; Length 347; Pred. No. 29; 4; Indels 1; Mismatches 4; Indels 347 AA; 37988 MW; FDB4CDC982F1B707 CRC64; Isold=Q8N919-2; Sequence=VSP\_008354;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the Deltex family.
-!- SIMILARITY: Contains 1 RING-type zinc finger. similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; IsoId=Q8N919-1; Sequence=Displayed; SEQUENCE OF 4-201 FROM N.A. (ISOFORM 1). [3] IN VITRO UBIQUITIN LIGASE ACTIVITY. EMBL, AK092085; BAC03801.1;
EMBL, AK094385; BAC04344.1;
EMBL, ALS31941; CAD38593.1;
EMBL, HGNC:2447; DTX3
INEEPPO; IPR001841; Znf\_ring.
Pfam; PF00097; Zf-C3HC4; 1.
SWART; SM00184; RING; 1.
PROSITE; PS00618; ZF\_RING 1; 1. Query Match 61.5%; Sco Best Local Similarity 66.7%; Pro Matches 10; Conservative 1; Nat. Genet. 36:40-45(2004). 151 164 122 1 Zinc-finger Name=1; SEQUENCE VARSPLIC ZN FING DOMAIN

2 PRPPFFFPRLPPRI 16

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and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Regulator of Notch signaling, a signaling pathway involved in cell-cell communications that regulates a broad spectrum of cell-fate determinations. Probably acts both as a positive and negative regulator of Notch, depending on the developmental and cell context. Functions as an ubiquitin ligase protein in vitro, suggesting that it may regulate the Notch pathway via some ubiquitin ligase activity (By similarity).

-!- SUBUNIT: Homomultimer. May form a heteromultimer with other members of the Deltex family. Interacts with NOTCH1.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

-!- TISSUE SPECIFICITY: Strongly expressed in testis and brain. Weakly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed in kidney.

DEVELOPMENTAL STAGE: In the CNS, it is expressed in the developing neural tube starting from E10.5 in the spinal cord and around E11.5 in the telencephalon. Expressed ubiquitously throughout the spinal cord and telencephalon during neurogenesis. Expressed throughout the developing retina at E15.5. Not expressed in the somite or presomite during somitogenesis. Expressed in the
                                                                                                                                                                                                                                                                                                   MEDLINE-21123790; Pubmed-11226752; DOI=10.1016/S0736-5748(00)00071-X; Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S., Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the Deltex family.
SIMILARITY: Contains 1 RING-type zinc finger.
CAUTION: Ref.2 sequence differs from that shown due to a chimeric
                                                                                                                                                                                                                                                                                                                                                               "Murine homologs of deltex define a novel gene family involved in vertebrate Notch signaling and neurogenesis."; Int. J. Dev. Neurosci. 19:21-35(2001).
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND
                                                                                                       10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
2b-tex protein 3 (Deltex-3) (Deltex3) (mDTX3)
Name=Dtx3;
                                                                              347 AA
139 PPPPPLPPPL 153
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                       Okano H., Matsuno K.;
                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                           DTX3 MOUSE (080V91, 09ER06;
                                                                                                                                                                                                                                                                                        MULTIMERIZATION
                                                             DTX3_MOUSE
                                              RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                    SWART; SM00184; KING; L. PROSITE; PROSITE; PROSITE; PROSITE; PS50089; ZF RING 2; 1. Metal-binding; Notch signaling pathway; Zinc; Zinc-finger. ZN_FING 164 205 RING-type.

ZN_FING 164 205 Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 59; DB 1; Length 347; 66.7%; Pred. No. 29; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 26, 2005, 05:18:35
                                                                                                                                                                 EMBL; AB015425; BAB18942.1; -.
EMBL; BC044779; AAH44779.1; ALT_SEQ
                                                                                                                                                                                                                          InterPro; IPR011046; WD40 like.
InterPro; IPR001841; Znf ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 PPPPPLPPPLPPRL 153
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Matches 10; Conservative
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                                                                                                                                           October 26, 2005, 05:02:04; Search time 16.4364 Seconds (without alignments) 72.667 Million cell updates/sec
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Sequence 66,
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Sequence 4, A
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Sequence 3,
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1: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata1/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/FB_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-722-825-66
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US-08-030-777A-2

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US-08-130-722-1

US-08-119-066-1

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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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96
1 RPRPPPFPPRLPPRI 16
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Perfect score:
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79 1 US-08-487-359-1 79 1 US-08-487-359-2 79 1 US-08-487-359-3 79 1 US-08-22-798A-1 79 1 US-08-22-798A-3 79 1 US-08-22-798A-3 79 1 US-08-22-798A-3 79 1 US-08-22-798A-3 70 1 US-08-22-798A-3 70 4 US-09-248-796A-21400 511 4 US-09-248-796A-8182 79 1 US-08-489-039A-8182 79 1 US-08-22-798A-4 97 4 US-09-489-039A-10835 433 4 US-09-489-039A-10835 433 4 US-09-489-039A-10835	IGNMENTS LATION OF REPERFUSION E 400 S, Version #1.30 975 306	000	UPPRI 16
229 229 331 331 331 332 333 334 335 337 337 338 337 338 338 338 338	RESULT 1  US-09-024-975-3  Sequence 3, Application US/09024975  Sequence 3, Application US/09024975  Sequence 3, Application US/09024975  Patent No. 6133233  GENERAL INFORMATION:  APPLICANT: ROSS, CHRISTOPHER R. APPLICANT: SHI, JISHU  TITLE OF INVENTION: PEPTIDE MODU TITLE OF INVENTION: SUIT CORRESPONDENCE ADDRESS:  ADDRESSEE: HOVEY, WILLIAMS, TII STREET: 2405 GRAND BLVD., SUIT CITY: KANSAS CITY STREET: 2405 GRAND BLVD., SUIT CITY: KANSAS CITY STREET: AND COUNTRY: USA ZIP: 64108 COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: TROPEMATION: PEPTING SYSTEM: PC-DOS/MS-DO SOFTWARE: PATENTIN NUMBER: US/09/024, FILING DATE: CLASSIFICATION DATA: ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION NUMBER: 25.262 FILING DATE: 18-FEB-1997 ATTORNEY/AGENT INFORMATION: TELEPHONE: 816/474-9057 INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acide TYPE: TINEAT	Query Match Best Local S. Matches 16	Qy 1 RPRPPFFPPRLPPRI

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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 25262
REFERENCE/DOCKET NUMBER: 2362
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (816) 474-9050
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 26 amino acids
amino acid
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MEDIUM TYPE:
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Patent No. 6713605

GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Bhi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
(ORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREE: 2405 Grand Blvd., Ste. 400
(ITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-UOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION S30
PROOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9050
TELEPHONE: CHARATTERICES:
SEQUENCE CHARATTERICES:
                                                                                            Sequence 5, Application US/08930777A
Patent No. 6713605
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blccha, Frank
APPLICANT: Blccha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 96; DB 4; I 100.0%; Pred. No. 2.1e-05;
                                                                                                                                                                                                                                                                               ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City STATE: Massouri
                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 64108
COMPUTER REARABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
1 RPRPPFFPPRLPPRI 16
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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GY: linear
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Sequence 2, Application US/08419066
SEQUENCE 3006
TITLE OF INTENTION: SNTHHETIC ANTIMICROBIAL PEPTIDE NUMBER OF SEQUENCES: 2
CORRESPEDIDENCE ADDRESS: 2
CORRESPEDIDENCE ADDRESS: 3
ADDRESSE: Collins, Hovey, Williams, Timmons ADDRESSE: Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
COMPUTER: FIGHPY CERN
COMPUTER: FIGHPY CERN
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APPLIL 10, 1996
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: COllins, John MAER: 26,262
REFRENCE/DOCKET WUMBER: 26,262
RELEPRANICATION INFORMATION:
TELLEPAX: (816) 474-9057
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRARACTERISTICS:
LEMTH: 23 aniho acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
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ZIP: 64108
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Patent No. 6133233
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSS, CRR.STOPHER R.
APPLICANT: SHI, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                Length 26;
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
CONTY: MO
CONTY: MO
CONTY: CANSAS CITY
CONTY: MO
CON
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100.0%; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                Score 96; DB 2;
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLING, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RPRPPPFPPRLPPRI 26
                                                                                                                                                // ANTI-SENSE: NO
// FRAGMENT TYPE: N-terminal
US-08-419-066-2
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Matches 16; Conservative
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STRANDEDNESS: single
                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-024-975-2
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Gaps
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patent No. 6794490

GENERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
FILE REPREBACE: C060

CURRENT FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTH: 38
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GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Blecha, Frank
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVERTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/POCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 96; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RPRPPFFFPRLPPRI 16
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                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 amino acida
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; Sequence 2, Application US/08930777A

RESULT 6 US-08-930-777A-2

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CORRESPONDENCE ADDRESS:
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; Sequence 1, Application US/08310722
; Patent No. 5654273
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
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Sequence 1, Application US/08162052

Sequence 1, Application US/08162052

Sequence 1, Application US/08162052

GENERAL INFORMATION:
APPLICANT: BOWAN, Hans G
APPLICANT: BOWAN, Hans G
APPLICANT: MUTT, Viktor
APPLICANT: BOWAN, Hans G
APPLICANT: JOANNALL, Hans
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREET: STREE
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Local Similarity 100.0%; Pred. No. 4.7e-05;
1es 16; Conservative 0: Mismatral-
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                                       1 RPRPPPFFPPRLPPRI 16
                                                                                                   11 RPRPPFFPPRLPRI 26
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STRANDEDNESS: sir
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Matches
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ADDRESSE: Parter al. Pabet

STREET: 1100 Peachtree Street, Suite 2800

CITY: Aclanta

STREET: 1100 Peachtree Street, Suite 2800

CITY: Aclanta

STREET: 100 Peachtree Street, Suite 2800

CONFART: USA

CONFART: USA

CONFART: STREET: STREET: PROPON disk

CONFART: STREET: S
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Gaps

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Length 39 0; Indels

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Sequence 1, Application US/09024975
Sequence 1, Application US/09024975
Patent No. 613323
GENERAL INFORMATION:
APPLICANT: BLECHA, FRANK
APPLICANT: BLECHA, FRANK
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 3; Length 39; 100.0%; Pred. No. 4.7e-05; Live 0; Mismatches 0; Indels
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CIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATONEY/AGENT INPORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REGISTRATION NUMBER: 25,262
REFERENCE/POCKET NUMBER: 25,85-A
                                             AUTHORS: Lee, Jong-Youn
JUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
MITHORS: Jornvall, Hans
JILLS: No. 5863897el Polypeptides And Their Use
JONGRAL: PCT WO 92/22578
JATES: No. 5863897el Polypeptides And Their Use
JONGRAL: PCT WO 92/22578
JATES: No. 5863897el Polypeptides And Their Use
JONGRAL: PCT WO 92/22578
JATES: No. 5863897el Polypeptides And Their Use
JONGRAPH: No. 5863897el No. 1: FROM 1 TO 39
US-08-728-333-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS STREET: 2405 GRAND BLVD., SUITE 400 CITY: KANSAS CITY STATE: MO
                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 2; 1
100.0%; Pred. No. 4.7e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RPRPPFFPPRLPPRI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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                     ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Yo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-024-975-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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APPLICANT: Gallo. Richard L.
APPLICANT: Klagsbrun, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 2; Length 39; 100.0%; Pred. No. 4.7e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
COUNTRY: Georgia
COUNTRY: 0309-4530
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/310,722
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELECHONE: (404)-815-6508
TELEPHONE: (404)-815-6555
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08728333 Patent No. 5863897
                                                         FLLING DAILS
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 2362
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RPRPPFFPPRLPPRI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
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SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                              ACECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENS
                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Gaps

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COUNTRY: USA ZAREES: ERNNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: NY COUNTRY: USA ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM COMPALIBLE OFFRATING SYSTEM: DOS SOFTWARE: FASTENG VERSION 2.0
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/179,558 FILING DATE: 27-OCT-1998 CLASSIFICATION S14 PRIOR APPLICATION NUMBER: US. 09/060,470 FILING DATE: 15-ARR-1998 FILING DATE: 13-OCT-1997 ATTONNEY AGENT INFORMATION: NAME: COTUZZI, LAURA A REGISTRATION NUMBER: 30,742
                 FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (404)-873-8794
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENGE: NO
PUBLICATION INFORMATION:
NITHERORY ING
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Boman, Hans G.
Mutt, Viktor
Jornvall, Hans
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
AUTHORS:
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US-09-179-558-66
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GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporaton
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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  useron-sou-///A-1

Sequence 1, Application US/08930777A

Patent No. 6713605

GENERAL INFORMATION:

APPLICANT: Blecha, Frank
APPLICANT: SAI, Jishu
STREET: 2405 Grand Blvd., Ste. 400

CITY: Kanasa City
STREET: Alssouri
CONNTRY: Us.A.
ZIP: Missouri
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Batentln Release #1.0, Version #1.25

COMPUTER: Patentln Release #1.0, Version #1.25

COMPUTER: Patentln Release #1.0, Version #1.25

CURRENTING SYSTEM: US/08/930,777A

PILING DATE: October 8, 1997

CLASSIFICATION NUMBER: US/08/940474

FILLING DATE: April 10, 1996

CLASSIFICATION NUMBER: 26,262

REGISTRATION NUMBER: 26,262
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100.0%; Pred. No. 4.7e-05;
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STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RPRPPPFFPPRLPPRI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-08-930-777A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
GY: linear
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hes 16; Conserv
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-08-930-777A-1
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Matches
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Gaps
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Sequence 66, Application US/09179558
Patent No. 6180612
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
APPLICANT: Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING
TITLE OF INVENTION: ANINOGLYCOSIDE DERIVATIVES
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 5; Length 39; 100.0%; Pred. No. 4.7e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DATE: 12/23/92; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39 PCT-US95-12080-1
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Novel Polypeptides And Their Use JOURNAL: PCT WO 92/22578
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Search completed: October 26, 2005, 05:21:58 Job time: 17.4364 secs

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Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 2, Appli
                                                                                                                                                                October 26, 2005, 05:05:05; Search time 59.0545 Seconds (without alignments) 113.119 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/NSO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-611-147-5
US-10-014-147-3
US-10-651-147-3
US-10-014-147-2
US-10-014-147-2
US-09-733-742-1
US-09-733-742-1
US-09-733-55-1
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US-10-391-155-1
US-10-391-155-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1862994 seqs, 417510619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                       1 RPRPPFFPPRLPPRI 16
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Maximum DB seq length: 200000000
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Query
Match Length D
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                             Sequence:
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Sequence 6, Appli Sequence 1, Appli Sequence 18, Appl	44 4 0	Sequence 13	Sequence 2	6 Seguence 22465 6 Seguence 19061	Sequence 12657	sequence 34667	Sequence 22049	Sequence 1933	1 Sequence 2	Sequence 12852	Sequence 18950	Sequence 31607	Sequence 28514	Sequence 18013	s Sequence 10885	3 Sequence 2045	quence 102,	equence 102,	equence 102,	392	edneuce	e 392,	quence 1473,	S	Sequence 2589	Segmence
US-10-391-1 US-10-651-1 US-10-344-7	US-10-9 US-10-9	US-10-156-761-1	US-10-425-115-20018 US-10-425-115-26871	US-10-425-115-22465	US-10-437-963-1265	US-10-425-115-346	US-10-425-115-22049	US-10-43/-963-16934 US-10-767-701-51171	US-10-425-115-	US-10-437-963-	US-10-425-115-	US-10-425-115-	US-10-425-115-2	US-10-437-963-	US-10-437-963-1	US-10-437-963-20496	643-10	US-10-042-141-1	US-10-919-272-1	US-09-809-391-3	US-09-882-171-3	US-10-164-861-3	-925-300-14	US-10-424-599-2316	US-10-424-599-258	
39 15 39 15 42 16	444	V 1	91 16 153 16		4 ~	7	٦,	٦,	١.	-	-	Н	_	_	-	-	520 9	٦	Н	٦	521 10	Н		80 15	~	7
96 100.0 96 100.0 96 100.0	9000	78.1	68.8	65.6	64.6	64.6	64.6	64.6	63.5	63.5	63.5	63.5	0 62.5	0 62.5	0 62.5	0 62.5	0 62.5	0 62.5	0 62.5	0 62.5	2.5	0 62.5	0 62.5	5 62.0	9 61.5	61.5
12 13 14	15	118	19 20	21	23 23	24	25	26 27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	ς,	44	45

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RESULT.

US-10-014-147-5

Sequence 5, Application US/10014147

Publication No. US20030125249A1

GENERAL INFORMATION:
Shi, Jishu

TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBERS OF SEQUENCES: 9
CORRESPONDENCE 1900

TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBERS OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STRRET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City
STRATE: Missouri
COUNTY: U.S.A.

COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOMPUTER: EADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: DATE: PLOPS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: DC/USS6/04674
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/USS6/04674
APPLICATION NUMBER: PCT/
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Query Match 100.0%; Score 96; DB 14; Length 23; Best Local Similarity 100.0%; Pred. No. 0.00093; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                 APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
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TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REFERENCE/DOCKET NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
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Publication No. US20040043934A1
GENERAL INFORMATION:
                                                                                                                Sequence 3, Application US/10014147 Publication No. US20030125249A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 23 amino acids
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1 RPRPPPFFPPRLPPRI 16
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 16; Conservative 0; Mismatches 0. T-2-1.
                                                                                                                                                                                                                                                                                       100.0%; Score 96; DB 14; Length 16; 100.0%; Pred. No. 0.00068;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 64108
COMPUTER READABLE FORM:
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC COMPATIBLE
COMPUTER: 1EM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Colling, John
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
                                                                                                                                                                                                                                                                                                                                         Mismatches
  TELEPHONE: (816) 474-9050

TELEPAX: (816) 474-9050

TELEPAX: (1616) 474-9057

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acide

TYPE: amino acid

TYPE: amino acid

MOLECTLE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-014-147-5
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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TELEPHONE: (816) 474-9050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (816) 474-9057
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-651-147-5
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Gaps

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COUNTRY: U.S.A

1 RPRPPFFPPRLPPRI 16

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: ADDRESSEE: HOVEY, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 96; DB 15; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
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                                                                                       474-9057
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SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RPRPPFFPPRLPPRI 16
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                                                                                                                         INFORMATION FOR SEQ ID NO: 2
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                           (816)
                              TELECOMMUNICATION
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Publication No. US20030125249A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES:

CORRESPONDERS:

ADDRESSE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 15; 100.0%; Pred. No. 0.00093;
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9051
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY AGENT INFORMATION:
NAME: COlling, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-10-651-147-3
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Matches 16; Conservative
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US-10-014-147-2
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CITY: Magnolia
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Sequence 1, Application US/09739535;
Publication No. US20020058785A1;
GENERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS;
FILE REFERENCE: C060
CURRENT APPLICATION NUMBER: US/09/739,535;
CURRENT FILING DATE: 2000-12-15;
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SSCTWARE: Patentin version 3.1
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                                                                                                           Sequence 1. Application US/09738742
Publication No. US20020025924A1
GENERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
TITLE REFERENCE: C060
CURRENT APPLICATION NUMBER: US/09/738,742
CURRENT FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 9; Length 38; 100.0%; Pred. No. 0.0014;
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Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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11 RPRPPPFFPPRLPPRI 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Synthetic US-09-739-535-1
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 16; Conserve
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                                                                                                     -09-738-742-1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEME: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 07-Doc-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APril 10, 1996
ATTORNEY/AGBVI INFORMATION:
REGISTRATION NUMBER: 26,262
STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 23625-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
                                                                                     ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (816) 474-9
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.
Matches 16; Conservative
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                                              STATE: Missouri
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US-10-391-155-6
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APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION: Mechael for PR-39 peptide mediated
selective inhibition of IXBA degradation
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC
COMPUTER: Dell PC
COMPUTER: Dell PC
CORPATING SYSTEM: MS XP
SOFTWARE: Wordberfect version 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
CLASSIFICATION: UNKNOWN
ATTONNEY AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REGISTRATION NUMBER: 29,693
REGISTRATION NUMBER: 29,693
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 96; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels
REFERENCE/DOCKET NUMBER: BIS-044/D
        TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
TELECOMMUNICATION: 1
SEQUENCE CHARACTERISTICS:
TOPOLOGY: 110 ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-391-155-2; Sequence 2, Application US/10391155; Publication No. US20040009463A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RPRPPFFPPRLPPRI 16
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Gaps
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Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
WEDLUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC
OPERATING SYSTEM: MS XP
SOFTWARE: WordPerfect version 10
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APPLICANT: Blecha, Frank
Sit, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kanasa City
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET WUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
CLASSIFICATION: Unknown
                                                                                                                                                                                                   CORRESPONDENČE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Publication No. US20040043934A1
Sequence 6, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                             APPLICANT: Simons, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
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                                                                                                                                                                                                                                                                                 CITY: Magnolia
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SEQ ID NO 14
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APPLICANT: JORG FRITZ ET AL.

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and rathelicidin TITLE OF INVENTION: Vaccine which comprises at least on a derivative thereof FILE REFERENCE: SONNINGER: US/10/344,709C
CURRENT PILING DATE: 2003-02-14

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2000-08-17

RUMBER: OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 15; Length 39; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
            PRILING DATE: 28-Aug-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMERR: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION UNMERR: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COllins M.
REGISTRATION NUMBER: 26,262
REPERENCE/DOCKET NUMBER: 26,262
REPERENCE/DOCKET NUMBER: 26,262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFRAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
APPLICATION NUMBER: US/10/651,147
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-651-147-1
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Publication No. US20040170642A1
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Publication No. US20050107325A1
BENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RPRPPFFPPRLPPRI 16
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.0
Matches 16; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-014-147-6 92 1 RIPPGFPPRFPPRFP 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2105692 segs, 386760381 residues Searched:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1980s:\*
4: geneseqp200s:\*
5: geneseqp201s:\*
6: geneseqp2013s:\*
7: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description			-	-						_	-	_	_	_		_		Adj69455 Human hea	• •			Adl67258 Antimicro	Aaw01451 Leukocyte	Ade86114 Proline-a	Ad167256 Antimicro
SUMMARIES	ļ	a	AAW01449	ADE86117	ADL67259	AAR30491	AAR99121	AAR94446	AAW01446	AAW75722	AAB26888	AAB97280	AAB84690	ADD35364	ADE86112	ADL67254	ABB07714	ADR82250	AAB51194	ADJ69455	AAW01448	AAW75724	ADE86116	ADL67258	AAW01451	ADE86114	ADL67256
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Leukocyte	Proline/A	Proline-8	Antimicro	Arabidope	Human	Novel	Novel	Novel	Novel	Novel	Nove1	Novel	Novel	Antipsori	Human	Novel	Novel	Novel	Novel
Aaw01447	Aaw75723	Ade86113	Ad167255	Aay05824	Adc38726	Abo44410	Abo44402	Abo44394	Abo44386	Abo44407	Abo44399	Abo44391	Abo44383	Adn03630	Ad811120	Abo44409	Abo44401	Abo44393	Abo44385
AAW01447	AAW75723	ADE86113	ADL67255	AAY05824	ADC38726	ABO44410	ABO44402	AB044394	ABO44386	ABO44407	ABO44399	ABO44391	ABO44383	ADN03630	ADS11120	ABO44409	ABO44401	ABO44393	ABO44385
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26	56	26	. 26	213	260	741	769	801	829	894	922	954	982	1419	1981	2004	2032	2064	2092
62.0	62.0	62.0	62.0	62.0	6.09	6.09	60.9	6.09	60.9	6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09
57	57	57	57	57	95	9	95	26	95	95	98	26	26	95	99	92	95	25	26
26	27	28	29	30	3 1	32	33	34	3.5	3.6	3.7	38	6	4 0	41	4 2	43	4 4	45

### ALIGNMENTS

Leukocyte 02- production inhibitor peptide PR15. AAW01449 standard; peptide; 15 AA (first entry) 18-JUN-1997 AAW01449; RESULT 1 AAW01449 

Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; buds synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.

Synthetic.

WO9632129-A1

17-0CT-1996.

96WO-US004674. 10-APR-1996;

95US-00419066. 10-APR-1995; (UNIV ) UNIV KANSAS STATE RES FOUND.

Shi J; Blecha F,

WPI; 1996-476842/47.

Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes – using peptide(s) partic. based on antimicrobial PR-39.

Claim 12; Page 28; 45pp; English.

AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. These sequences, and PR39, can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (O2-) production. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte 02-

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production. The peptides can be used as medicaments for fighting hifection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of inhibiting leukocyte superoxide anion (O2-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or an eneutrophil, to a location, e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs the location.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   excessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                                                                                                                                                                                                                                                                                       Leukocyte superoxide anion; leukocyte O2- production; leukocyte attraction; proline-arginine-rich antimicrobial peptide; PR-rich antimicrobial peptide; neutrophil; wound site; infection; tissue damage; oxygen radical; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 92; DB 8; Length 15; 100.0%; Pred. No. 0.00018; Pred. o. Mismatches 0; Indels
                                                                                          Length 15
                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                      Proline-arginine (PR)-rich antimicrobial peptide PR-15.
                                                                                        Score 92; DB 2; I Pred. No. 0.00018; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 6; 24pp; English.
                                                                                                                                                                                                                    ADE86117 standard; peptide; 15 AA.
                                                                                                                ö
                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2001; 2001US-00014147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00419066.
                                             inflammatory disease states
                                                                                                                                       1 RIPPGFPPRFPPRFP 15
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                                                                                                                                                                                                                                                                 (first entry)
                                                                                       Ouery Match
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-059188/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shi J;
                                                                                                                                                                                                                                                                                                                                                                                          US2003125249-A1.
                                                                    Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-1995;
08-OCT-1997;
                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blecha F,
                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                          ADE86117;
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                                                                                                                                                                                           RESULT 2
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                                                                                                                                                                                            Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-15.
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                                                                                                                                                                 Antimicrobial peptide PR-39 analog PR-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; SEQ ID NO 6; 24pp; English.
                                                                                ¥
                                                                                ADL67259 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                       28-AUG-2003; 2003US-00651147.
                                                                                                                                                                                                                                                                                                                                                                   95US-00419066.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-225728/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blecha F, Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                           BLEC/) BLECHA F.
                                                                                                                                                                                                                                                                                US2004043934-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          SHI J.
                                                                                                                                                                                                                                                                                                                                                                   10-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1997;
                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                      20-MAY-2004
                                                                                                                                                                                                                                                                                                              04-MAR-2004
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                                                   RESULT 3
ADL67259
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1 RIPPGFPPRFPPRFP 15

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Gaps

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15; Conservative

Matches

AAR30491;

AAR30491

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AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be used to treat sexually transmitted diseases (STDS) caused by Chlamydia, HIV, herpese simplex virus, Neisseria gonnorhoeae or Candida infection. The peptides inhibit STDS by either killing the infectious organism, impeding the infection mechanism or interrupting the replication cycle of the organism. Squalamine (an aminosterol host defence molecule of the dog fish shark Squalus acanthias) and PGLa (a frog antimicrobial peptide) analogues may also be useful in inhibiting STD infection and transmission
                                                                                                                                                                                                                                                                                                                                                     Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by administering magainin antimicrobial or squalamine cpd. to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synducin; induction; expression; syndecan-1; syndecan-4; surface; mesenchymal cell; fibroblast; epithelial; Rr-39; treatment; stasis; decubitus; ulcers; keloids; skin burns; ischemic tisques; hypercoagulation states; prevention; tumour metastesis; restenosis; inhibition; angiogenesis; proliferation; endothelial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 92; DB 2; Length 39; 100.0%; Pred. No. 0.00044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synducin peptide (PR-39) induces syndecan expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                      Bedi
                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR94446 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 32; 60pp; English.
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                                                                             /note= "amidated"
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                                                                                                                                                                                                                                                                                      Williams
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                                                                                                                                                                                   95WO-US011675
                                                                                                                                                                                                                      94US-00305475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                        (MAGA-) MAGAININ PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                          Zasloff M,
                                                                                                                                                                                                                                                                                                                            WPI; 1996-179725/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39 AA;
                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1995;
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                                                                                                                                                                                                                      13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                               transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9609322-A2
                                                                                                                                                                                   13-SEP-1995;
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                                                                                                                                                   21-MAR-1996
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              Synthetic
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                                                                                                                                                                                                                                                                                          Jacob L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide was isolated from the small intestine of a pig. The small inestine is an important endocrine organ and many physiologically active peptides have been isolated from it. This peptide inhibits the growth of, and may kill, bacteria, pref. gram negative bacteria. This peptide or its thnctional derivatives may be used in human or veterinary medicine for therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-bacterial polypeptide - active against Gram negative bacteria.
                                                                                                                                                                                                                                                         small intestine; endocrine; gram negative; bacteria; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STD; sexually transmitted disease; HIV; human immunodeficiency virus; herpes simplex virus; HSV; Neisseria gonnorhoeae; Candida; Chlamydia; magainin; antimicrobial; squalamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR99121 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                               veterinary medicine; prophylactic.
                                                                                                      AAR30491 standard; peptide; 39 AA.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-SE000394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        91SE-00001838
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RIPPGFPPRFPPRFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boman HG, Mutt V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1996 (first entry)
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                          (revised)
                                                                                                                                                                                                                             Antibacterial peptide
                                                                                                                                                                                                                                                                                                                 Sus scrofa domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JOER/) JOERNVALL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-018080/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEE J.
BOMAN H G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                   W09222578-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1992.
                                                                                                                                                                       25-MAR-2003
12-MAY-1993
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(LEEJ/) (BOMA/) (MUTT/)

Lee J,

AAR99121

RESULT

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Gaps

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                                                                                                                                                                                                 syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.

fibroblasts and epithelial cells. The 36 N-terminal amino acids of the
peptide were found to be identical to the 36 N-terminal amino acids of PR
-39, a Pro and Arg rich antibacterial peptide previously found in porcine
intestine (W0922578). Synducins may be used in the treatment of stasis
and decubitus ulcers, keloids, skin burns, ischemic fissues and
hypercoagulation states, prevention of tumour metastasis, restenosis
inhibition and endothelial cell angiogenesis and proliferation induction.
expression following exposure to 5 % wound fluid, dbcAmP (1 mM), the
present peptide (10 microM) or a blank, to give respective cell surface
syndecan-4 values (moD/m in) of approx. 1.75, 1.70, 1.80 and 0.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; DNA synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
                                                                                                Modulating mesenchymal interaction by administration of synducin - used in the treatment of wounds, tumours, restenosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
                                                                                                                                                                            The present peptide is a synducin, which induces the expression of syndecan-1 and syndecan-4 on the surface of mesenthumal call,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 92; DB 2; Length 39; 100.0%; Pred. No. 0.00044; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukocyte O2- production inhibitor peptide PR39.
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                                                                                                                                                  Claim 4; Page 26; 34pp; English
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(CHIL-) CHILDRENS MEDICAL CENT.
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Matches 15; Conservative
                              Bernfield
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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This sequence represents the proline-arginine rich antimicrobial peptide PR39 requence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. This sequence, and the fragments of it shown in AAW0147-W01454, can be used in the method of the invention. The method of the invention. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte a peptide such as this sequence) capable of inhibiting leukocyte 02- production. The peptides can be used as medicaments for fighting infection by the peptides can be used as medicaments for fighting infection by the second of the inventing tissue damage at the contracting leukocytes to a wound site and restricting tissue damage at the contraction of the contracting tissue damage at the contraction of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 administration into a mammal's bloodstream reduce reperfusion injury production of reactive oxygen species, neutrophila adherence to reduchelium, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXP, where P is a requirement end X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reduction of reperfusion injury in temporarily occluded blood vessels - by administration of a peptide which is rich in proline or arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           eukocytes. They can also be used to develop products for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 92; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease states
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1998;
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16-FEB-1998;
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Gaps

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100.0%; Score 92; DB 3; Length 39; 100.0%; Pred. No. 0.00044;

0; Mismatches

1 RIPPGFPPRFPPRFP 15

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Query Match Best Local Similarity 100. Matches 15; Conservative

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ideally contain 4 or 6 of these motifs, and that a peptide should ideally contain 4 or 6 of these motifs, and that inhibitory activity is correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the neutrophil superoxide anion, and also the inhibition of neutrophil superoxide anion, and also the inhibition of neutrophil oxidase to some extent. All of the peptides also inhibited NADPH oxidase to some extent. All of the peptides also inhibit neutrophil oxidase activity. PR-39 is believed, to be the most potent endogenous produced, it can be suggested to be involved in eliminating or reducing the reperfusion injury induced adhesion and extraction of neutrophils.
                                                                                                                                                       The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                          Score 92; DB 2; Length 39;
Pred. No. 0.00044;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR-39 peptide used in angiogenesis control.
                                                                                                                                                                                                                                                                                                                                                                                     AAB26888 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myocardial ischaemia; proteasome.
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                    Sequence 39 AA;
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                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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PR-39; cathelin; inflammation; wound healing; myocardial infarction; proteasome; proteolysis; alpha7; peptide degradation; angiogenesis; anoxia; chronic myocardial ischaemia; heart tissue.

AAB97280 standard; peptide; 39 AA.

RESULT 10

(first entry)

09-AUG-2001

AAB97280;

PR-39 peptide

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Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39

C is a member of the the cathelin family of proteins, mature PR-39

C represented by the present sequence is 39 amino acids in length, and has been shown to play a role in several inflammatory events including wound consider the protein of proteasone mediated in consequence is allowed family of oligopeptides cause selective inhibition of proteasone mediated introduction to a target cell. PR-39 derived peptides are intracellular introduction to a target cell. PR-39 derived peptides are been to interact with at least the alpha? subunit of the proteasomes, and therefore alter the proteolytic activity of proteasomes such that contracts methods for the selective inhibition of proteasome mediated contraction of proteasome mediated includes methods for the selective inhibition of proteasome mediated contraction in proteolytic activity of proteins occurs. The invention contraction of proteasome mediated contraction in angiogenesis as required in living tissues and organs which have suffered angiogenesis as required in living tissues and organs which have suffered myocardial is schemal of heart tissues. Examples are the myocardian, skeletal or smooth muscle, artery or vein, lung, brain, the contraction or extremities. A particular example is after myocardial infarction or extremities. ö Gaps ö 100.0%; Score 92; DB 4; Length 39; 100.0%; Pred. No. 0.00044; 0; Indels 0; Mismatches Query Match (100. Best Local Similarity 100. Matches 15; Conservative Sequence 39 AA; 

This invention relates to a method for the stimulation of angiogenesis in situ within a targeted collection of viable cells. The method comprises introducing, into the cytoplasm, at least i member of the PR-39 oligopeptide collective, which interacts with cytoplasmic proteasomes. Part of the proteolytic activity of the proteosomes is selectively altered so as to stimulate angiogenesis. The method is used to induce angiogenesis in tissue that has suffered anoxia or infarction, e.g. myocardial infarction or chronic myocardial ischaemia, and also to study the mechanisms that control angiogenesis. The present sequence represents the PR-39 peptide from which peptide used in the method of the invention

Sequence 39 AA;

Stimulating angiogenesis in situ, useful e.g. for treating anoxia and infarction, by administering a PR-39 oligopeptide that regulates enzymatic activity of proteosomes.

WPI; 2000-628319/60

Simons M,

Disclosure; Page 21; 51pp; English

Stimulation of angiogenesis and inhibition of proteasome mediated degradation in cells, by introduction of PR-39 oligopeptide or its N-terminal fragments or their conjugates, for use in anoxia and infarction

Disclosure; Page 21; 52pp; English.

conditions

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

WPI; 2001-355179/37 Simons M, Gao Y;

06-OCT-2000; 2000WO-US027552.

25-OCT-1999;

WO200130368-A1.

03-MAY-2001

Unidentified.

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The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraccular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work symergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysplasia, iridial melanocyte hyperplasia, and hyperpigmentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukocyte superoxide anion; leukocyte O2- production; leukocyte attraction; proline-arginine-rich antimicrobial peptide; PR-rich antimicrobial peptide; neutrophil; wound site; infection; tissue damage; oxygen radical; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proline-arginine (PR)-rich antimicrobial peptide PR-39.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Maxey KM, Johnson J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention.
                                                                                                                                                                                                    02-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a PR-39 protein. The specification describes PR-39 derived peptides, which are used for selective inhibition of IxappaBalpha degradation within a targeted cell collection in-situ. The method is useful for selectively inhibiting IkappaBalpha protein degradation in situ, decreasing the activity of NFkappaB transcription factor and selective control of NFkappaB dependent gene expression in situ. The PR-39 derived peptides are useful in the treatment of myocardial infarction, chronic myocardial ischemia of heart disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selective inhibition of IkappaBalpha degradation within targeted viable cell collection, involves interacting PR-39 oligopeptide with IkappaBalpha and proteasomes, and altering proteolytic activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                          PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
myocardial infarction; chronic myocardial ischemia; heart disease;
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                                                                                                                                                                                                                                                                                  Amino acid sequence of a PR-39 protein.
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                                                                                                                                                            AAB84690 standard; protein; 39 AA.
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                                                25 RIPPGFPPRFPPRFP 39
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                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-441690/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200147540-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004
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Blecha F, Shi J;
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               US2004043934-A1
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                                                                                                                               10-APR-1995;
08-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of inhibiting leukocytes superoxide anion (02-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for a trracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                                                                                                                                                                                                           Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leucocyte ; superoxide anion; oxygen radical; proline-arginine ; antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil; infection; wound; tissue damage ; PR-39 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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/label= PR-26_peptide
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/label= PR-19_peptide
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|Tabel= PR-14_peptide
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/label= PR-16_peptide
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                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL67254 standard; peptide; 39 AA.
07-DEC-2001; 2001US-00014147.
                                     95US-00419066.
97US-00930777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide PR-39.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                           WPI; 2004-059188/06
                                                                                                                                                       Blecha F, Shi J;
                                                                                             (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39 AA;
                                                                                                                                                                                                                                                                       the location.
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                                     10-APR-1995;
08-OCT-1997;
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ADL67254
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The invention relates to inhibiting leucocyte superoxide anion (02-)

production using a naturally occurring proline-arginine (PR)-rich

artimicrobial peptide known as PR-39 and its truncated analogs. The

method comprises contacting leucocytes with the peptide comprising 39 or

method comprises contacting leucocytes with the peptide inhibits the activity

compression and anion production. The peptide inhibits the activity

of NADPH oxidase responsible for anion production, by binding to Src

compression of p47phox, which is a 47 kba cytosolic protein

compression of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or

portine leucocyte and the mammalian leucocyte is neutrophil. Another

comprise also disclosed which employs a PR-39 analog that comprise 16

method is also disclosed which employs a PR-39 analog that comprise 16

comprise and the sum of the proline and arginine residues in the

effective peptide is at least 6 or 74 % of the total number of amino

completed are least 6 or 17 % of the total number of amino

completed are arginine residues. The method of the invention is useful

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine, cathelicidin, antimicrobial, immunostimulant, immune response; antigen presenting cell; adjuvant; porcine; PR-19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1; 24pp; English
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28-AUG-2003; 2003US-00651147.
                                                                                                                95US-00419066.
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The invention relates to a vaccine comprising at least one antigen and at least one cathelicidin derived antimicrobial peptide or its derivative. The vaccine is useful for active immunization, especially of humans or animals without protection against the specific antigen. The cathelicidin derived antimicrobial peptide is useful in the preparation of an adjuvant for enhancing the immune response to at least one antigen, where the adjuvant enhances the uptake of at least one antigen in antigen presenting cells (APC), and the adjuvant is added to the vaccine. Sequences ABB07708-15 represent C-terminal fragments of antimicrobial peptides of the cathelicicidin family
                                                                                                                                                                                                                                                                         Vaccine for active immunization or for preparing an adjuvant for enhancing an immune response to at least one antigen, comprises at least one antigen and at least one cathelicidin derived antimicrobial peptide.
                                                                                                                                                                                         Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
                                                                                                                                                  (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 65pp; English.
                                                                                                        17-AUG-2000; 2000AT-00001416.
                                                             17-AUG-2001; 2001WO-EP009529.
                                                                                                                                                                                                                                    WPI; 2002-269154/31.
                   21-FEB-2002.
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Sequence 42 AA;

Gaps . 0 100.0%; Score 92; DB 5; Length 42; 100.0%; Pred. No. 0.00047; tive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Similarity Matches 15; Conserv

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1 RIPPGFPPRFPPRFP 15 

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Search completed: October 26, 2005, 05:12:08 Job time : 60.0455 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 26, 2005, 05:00:14 ; Search time 11.1818 Seconds (without alignments) 129.071 Million cell updates/sec

US-10-014-147-6 92 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RIPPGFPPRFPPRFP 15 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SUMMAKIES	Description	2	0 embryo-specifi		hypothetical F	cathelin-l				7	7	7 spliceosome-ass	retinoblastoma	collagen alpha	collagen alpha	collagen alpha	collagen al	dynamin 2 -	dynamin II	dynamin				proline-rich	proline-rich	proline-rich	5 proline-rich	7 proline-rich	timethorized archite
SOR	. <b>f</b>	S68232	T48490	JC4305	T48008	\$57330	S40463	T00206	T30351	T42727	D84672	JC5437	A57640	823779	A34246	823298	S15435	A36878					A54964	A29149	A30496				1120004
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d	Query Match	100.0	62.0	59.8	ന	58.2	58.2	57.6	57.6	57.1	56.5	56:5	56.0	55.4	55.4	L)	55.4	55.4	55.4	55.4	55.4	54.3	53.3	52.7	52.7	52.7	52.7	52.7	נ
	Score	92	57	55	54		53.5	23	53	52.5	52	52	51.5	51	51	51	51	51	51	51	51	20	49	48.5	48.5	48.5	48.5	48.5	0.7
•	Result No.		8	m	4	S	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	. 25	26	27	ć

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T32500 JE0284	S09779 S19595	A40513 T01561	D72711	105584 S64945	T02445 JC5669	T52524	S44457	T29265	S74287	A40315
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233	322 994	218	191	485 485	554 587	609	997	1357	259	1026
52.2	52.2	51.6	51.1	51.1	51.1	51.1	51.1	51.1	50.5	50.5
4.4 8.8	4 4 8 8	47.5	74.	7.4	744	47	47	47	46.5	46.5
30 31	332	3.4 3.5	36	37	3.9 0.4	41	42	43	44	45

### ALIGNMENTS

	א מאווים
	868232 antimicrobial protein PR-19 precursor, cathelin-associated - pig
	in PR-39
	C;Species: Sus scrots domestica (domestic ply) C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
	C;Accession: S68232; JN0899; 147138; S19363 R;Zhao, C.; Ganz, T.; Lehrer, R.I.
	FEBS Lett. 376, 130-134, 1995
	A;Title: Structures of genes for two cathelin-associated antimitiobial peptides: Propings A:Reference number: S68232; MUID:96105365; PMID:7498526
	A; Accession: S68232
	A;Status: transtation not snown A;Molecule type: DNA
	A; Residues: 1-172 <zha></zha>
	A)Crossreteraces: UNIEKOLTBUOG4; EMBL:A89201; NID:G1105150; FIDN:Unrotatoring tronscriptoring to the state of
	A.Storici, P.; Zanetti, M.
	Biochem. Biophys. Res. Commun. 196, 1058-11065, 1993. ***********************************
	A.Reference number: JN0899; MIID:94071853; PMID:8250863
	A, Accession: JN0899
	A; Molecule type: mRNA
	A;Residues: 1-20, A', 22-1/2 SID> A;Residues: 1-20, A', 22-1/2 SID> A: Crandes: 1-20, A', 22-1/2 SID>
_	A. Randrimental source: bone marrow cells
	R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome
	Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
	A; Title: Structure of the gene for porcine peptide antiblocic PK-39, a cachelin gene rans
	A;KeTePeonce Tulmoer: 14/138; Mull:39350/210; Fill:/Oc.43/4
	A:Status: oreliminary: translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
_	A, Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <gud></gud>
	A)Cross references: EMBL: X87286; NID: 9829462; PIDN: CARAGOGGAT; FID: SQLUDIZACOTACT; TO JOSEPHVALLE TO TOTAL TO THE TOTAL TO THE TOTAL T
	K;Agenberrn, b; hee, u.r.; bergman, r.; carigure, r.; commun; r.c.; r.c.; r. r.; Rinchem, 202, 849-854, 1991
	Airitle: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of the
	A; Reference number: \$19563; MUID:92111534; PMID:1765098
	A.Accession: \$19563
	Ajmoleoule Type: process Ajmoleoule Type: process
	A Nacimate 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	C. Genetics:
	A,Gene: PR39
	A; Introdus: 66/3; 128/3; 128/3; 128/3; homology
	C,Supertramily: carterin; cystatin; uniquotoy; C.kovonrds, amidated carboxvl end; antibacterial
	P;1-29/Domain: signal sequence #status predicted <sig></sig>
	F;22-129/Domain: cystatin homology <tys> F:30-130/Domain: propeptide #status predicted <pro></pro></tys>
_	Fil31-169/Product: antimicrobial protein PR-39 #status experimental <mat></mat>

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Nilternate names: antimicrobial peptide; prophenin-1
C; Species: Sus scrofa domestica (domestic pig)
R; Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A; Title: Molecular cloning and identification of a novel porcine cathelin-like antibacten A; Reference number: S57330; MUID:96042752; PMID:7576250
A; Rocession: S57330
A; Molecule type: mRNA
A; Residues: 1-212 <STR>
A; Cross-references: UNIPROT:P51524; GB:X86031; NID:gl006756; PIDN:CAA60023.1; PID:gl00675; R; Harwig, S. S. L.; Kokryakov, V. N.; Swiderek, K. M.; Aleshina, G. M.; Zhao, C.; Lehrer, R. I.
FEBS Lett. 362, 65-69, 1995
A; Reference number: S68726; MUID:95212585; PMID:7698355
                                                                                                                                                                                                                                             hypothetical protein T17J13.120 - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Jate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 (C.Jacession: T48008 (M. M. Meller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, Submitted to the Protein Sequence Database, February 2000 A; Reference number: Z24482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)
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A,Cross-references: UNIPROT:Q9M1Q8; EMBL:AL138651
A,Experimental source: cultivar Columbia; BAC clone T17J13
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0; Mismatches
  Mismatches
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Pred. No.
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C; Superfamily: cathalin; cystatin homology
C; Keywords: antibacterial
F; 6-113/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 PPNFPGPRFPPPNFPGPRFP 163
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64.3%;
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  Conservative
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Best Local Similarity
9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: T48008
A,Status: preliminary
A,Molecule type: DNA
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A; Introns: 137/3
A; Note: T17J13.120
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  Matches
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N;Alternate names: protein T28J14.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Datesion: T48490
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lesubmitted to the Protein Sequence Database, April 2000
A;Reference number: 224493
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A;Cross-references: GDB:696233
A;Map position: 9q12-9q12
A;Map position: 9q12-9q12
C;Superfamily: human dynamin II; pleckstrin repeat homology
C;Keywords: GTP binding: membrane trafficking; nucleotide binding; P-loop; phosphoprotei
E;38-45/Region: nucleotide-binding motif B
F;308-50/Nomain: protein kinase C substrate #status predicted <PKC>
F;518-619/Domain: pleckstrin repeat homology <PLK>
F;518-619/Domain: pleckstrin repeat homology <PLK>
F;116-126,760/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicte
F;116,126,760/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: JC4305
R;Diatloff-Zito, C:; Gordon, A.J.E.; Duchaud, E.; Merlin, G.
A;Title: Isolation of an ubiquitously expressed cDNA encoding human dynamin II, a member
A;Reference number: JC4305; MUID:96011652; PMID:7590285
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  F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following
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A;Residues: 1-866 -DDA>
A;Cross-references: GB:135983
C;Comment: This protein is a cytoskeletal protein that functions in endocytosis and
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                                                         Length 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%; Score 57; DB 2; Length 213;
69.2%; Pred. No. 1.3;
iive 0; Mismatches 4; Indels
                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9LYP6; EMBL:AL163652
A;Experimental source: cultivar Columbia; BAC clone T28J14
                                                      100.0%; Score 92; DB 2; 100.0%; Pred. No. 3.1e-05;
                                                                                                            0; Mismatches
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                                                      Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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A;Molecule type: DNA
A;Residues: 1-213 <BEV>
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A;Introns: 28/3; 65/3
A;Note: T28J14.130
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hypothetical protein At2g27390 [imported] - Arabidopsis thaliana cypothetical protein At2g27390 [imported] - Arabidopsis thaliana (mouse-ear cress) C;5pcties: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: D84672 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: D84672 S: Roule, S.; Rounsley, S.D.; Shan, N.I.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h R;Lin, X.; Kaul, S.; Roule, S.; Rounsley, S.D.; Shan, Y. Shan, N.; Shan, N.; VanAken, S.E.; Umayam, L.; Tallon, L.; Nature 402, 761-768, 1999
Nattle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Accession: D84672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-1560 <WIT>
A;Residues: 1-1560 <WIT>
A;Residues: 1-1560 <WIT>
A;Residues: 1-1560 <WIT>
C;Genetics: strain Balb/C
C;Genetics:
                                                                                                                                                                             CjAccession: T30351
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrn Virology 253, 17-34, 1999
Ajricle: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di Ajreference number: Z20836; MUID:99124785; PMID:9887315
                                                                            mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdWNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation potential related protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1029 <KUZ>
A;Cross-references: UNIPROT:Q9YMX0; EMBL;AF081810; PIDN:AAC70189.1
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80.0%; Pred. No. 21;
ative 1; Mismatches
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R;Witte, M.M.; Scott, R.E.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z22246
A;Accession: T42727
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; Pred. No. 37;
3; Mismatches
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Best Local Similarity 80.00,
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Matches 9; Conservative
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A;Molecule type: DNA
A;Residues: 1-134 <STO>
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C;Function:
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R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A;Reference number: S57330; MUID:96042752; PMID:7576250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Anolecule type: mRNA
A;Residues: 1-228 <STR>
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
R;EBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen
A;Reference number: S68232; MUID:96105365; PMID:7498526
prophenin (PP-2) precursor - pig
Nalternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 846463; 85731; 86823
R;Pungercar, J; Strukelj, B; Kopitar, G; Renko, M; Lenarcic, B.; Gubensek, F.; Turk,
FEBS Lett. 336, 284-288; 1993
A;Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
A;Reference number: 840463; MUID:94085623; PMID:8262247
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T00206
R;Chiba, S.; Satou, Y.; Nishikata, T.; Satoh, N.
submitted to the EMBL Data Library, November 1997
A;Description: Isolation and characterization of cDNA clones for tissue-specific genes
A;Reference number: Z14123
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A;Status: translated from GB/EMBL/DDBJ
A;Actus: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-741 <CHI>A;Cross-references: UNIPROT:015999; EMBL:AB008818; PIDN:BAA23597.1
C;Superfamily: Ciona savignyi epidermis-specific protein 1; trefoil homology F;568-610/Domain: trefoil homology <TRF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X89202; NID:g1165148; PIDN:CAA61488.1; PID:g1165149
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Best Local Similarity 60.0%; Pred. No. 3.8;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.6%; Score 53; DB 2; Length 741; Best Local Similarity 72.7%; Pred. No. 15; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introvens: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
F;1.29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-228/Product: prophenin (PF-2) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epidermis-specific protein 1 - Ciona savignyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 PENFPGPRFPPPNFPGPRFP 189
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726 IPPGYPPNTPP 736
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A,Molecule type: mRNA
A,Residues: 1-228 <PUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-228 <ZHA>
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56.5%;

Query Match
Best Local Similarity 60.0
Matches 9; Conservative

RESULT 11

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Mismatches Score 52; Pred. No.

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C;Accession: $23779 Forther or the continue of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: $23298
R;Ninomiya, Y:, Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McC? maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre? A;Fille: The molecular biology of collagens with short triple-helical domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g13599: C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology F;616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>
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R;Yamaguchi, N; Benya, P.D.; van der Rest, M.; Ninomiya, Y.
B;OL. Cchem. 264, 16022-16029, 1989
A;Title: The cloning and sequencing of alphal(VIII) collagen cDNAs demonstrate that type omains similar to those of type X collagen.
A;Reference number: A34246; MUID:89380199; PMID:2476437
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A; Residues: 1-744 < YAM>
A; Cross-references: UNIPROT: P14282; GB: U05042; NID: g164895; PIDN: AAA31204.1; PID: g164896
A; Cross-references: UNIPROT: P14219; Carboxyl-terminal homology
C; Superfamaily: collagen alpha 1(VIII) chain; predicted < SIGS
F; 21-744/Product: collagen alpha 1(VIII) chain #status predicted < MAT>
E; 21-117/Region: amino-terminal nonhelical
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collagen alpha 1(VIII) chain precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>
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Pred. No. 27;
3; Mismatches
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              398 LPPGVPPPQFSPQFP 412
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Best Local Similarity 50.vv
Best Local 7; Conservative
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Best Local Similarity
7; Conserve
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A; Residues: 1-743 <MUR>
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C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57640
R;Sakai, Y.; Saijo, M.; Coelho, K.; Kishino, T.; Niikawa, N.; Taya, Y.
A;Title: CDNA sequence and chromosomal localization of a novel human protein, RBQ-1 (RBE)
A;Reference number: A57640; MUID:96129310; PMID:8595913
A;Cross-references: UNIPROT:Q9XIP3; GB:AE002093; NID:g5306259; PIDN:AAD41991.1; GSPDB:GN C;Genetics:
C;Genetics:
A;Gene: At2g27390
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: JC5437.
R;Tanaka, Y.; Ohta, A.; Terashima, K.; Sakamoto, H.
R;Tanaka, Y.; Ohta, A.; Terashima, K.; Sakamoto, H.
R;Tanaka, Y.; Ohta, A.; Terashima, K.; Sakamoto, H.
A;Title: Polycistronic expression and RNA-binding specificity of the C. elegans homologu
A;Reference number: JC5437; MUID:97306058; PMID:9163526
A;Accession: JC5437
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A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: 1.388 - TAN>
A;Cross-references: 1.388 - TAN>
A;Cross-references: UNIPROT:Q17352; GB:U24189
C;Comment: This protein is a subunit of splicing factor SF3b and is involved in U2
C;Superfamily: ribonucleoprotein repeat homology
F;14-81/Domain: ribonucleoprotein repeat homology <RRM4>
F;101-169/Domain: ribonucleoprotein repeat homology <RRM2>
F;101-169/Domain: ribonucleoprotein repeat homology <RRM2>
F;260-388/Region: proline-rich
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C;Species: Caenorhabditis elegans
C;Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 16-Aug-2004
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RESULT 12

Query Match
Best Local Similarity 60.0
Matches 9; Conservative

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56.0%; Score 51.5; I 60.0%; Pred. No. 30; ive 3; Mismatches

Query Match Best Local Similarity Matches 9; Conserv

2 IPPGF-PPRFPPRFP 15

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C; Keywords: tandem repeat; zinc F;79-129/Domain: RING finger homology <RNG>

A,Cross-references: GDB:626076 A;Map position: 16p12-16p11.2 C;Keywords: randm

A; Molecule type: mRNA A; Residues: 1-948 <SAK> A; Status: preliminary A; Accession: A57640

A,Accession: S23298
A,Status: prelimary
A,Molecule type: DNA
A,Residues: 1-744 <NIN>
A,Crose-references: UNIROT:Q7LZR2
C,Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
P;617-743/Domain: complement Clq carboxyl-terminal homology

Query Match 55.4%; Score 51; DB 1; Length 744; Best Local Similarity 50.0%; Pred. No. 27; Matches 7; Conservative 3; Mismatches 4; Indels

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Search completed: October 26, 2005, 05:20:01 Job time: 13.1818 secs

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Q81271 arabidopsis
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G61135 dictyosteli
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G67vv4 oryza sativ
Q8vpb5 homo sapien
Q8upb5 homo sapien
Q8upb5 homo sapien
Q8upb5 homo sapien
Q8upb6 homo sapien
Q8upb8 homo sapien
Q8upb8 homo sapien
Q8upb8 homo sapien
Q8upb8 homo sapien
Q740x0 mycobacteri
Q740x0 mycobacteri
Q72ue4 brachydanio
Q6fn08 candia gla
P51525 sus scrofa
Q6fn08 mus musculu
Q91w60 mus musculu
Q91w60 mus musculu
Q91w60 mus musculu
Q91w60 mus musculu
Q91x69 mus musculu
Q91x60 mus musculu
Q8c7k5 mus musculu
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                                                               October 26, 2005, 04:52:03; Search time 51.9545 Seconds (without alignments) 147.844 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                            1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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QUUPHS
QBUUPHS
QBUUPHS
QBUUPHS
DNV2_HUMAN
QCNSHV3
QOYSHV3
QOYSHV3
QOT133
QC1133
QC1133
QC1133
QC1133
QFNO8
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PPFI_PIG
PPFI_PIG
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Q81LQ0
Q81LQ1
Q91Z71
Q94K23
Q91LYP6
O61134
Q67W44
Q67W44
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Q8C7K5
O54882
Q8C7G9
Q6ZH25
Q91Z39
Q6ESK7
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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92
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mus musculu	Q80w14	Q80W14.	7	890	'n	26	52	45
mus musculu	60AM60	Q9WVC9	~	873	٠.	56.5	52	44
homo sapie		Q6NWY9	~	871	'n	56	52	43
homo sapien	OBuczl	QBNCZ1	7	828	'n	56.	25	42
homo sapie	O6p109	Q6PI09	7	788	'n	26	25	41
neurospora	07ryv7	Q7RYV7	~	541	'n	99	52	40
_	017352	017352	~	398	'n	56.	52	39
	QBtBn6	OSTBN6	7	388	'n	26.	25	38
	065790	Q657Y0	~	236	'n	56.	52	37
	O6 zwb3	Q6ZWB3	~	195	'n	56.	25	36
	09x1p3	Q9XIP3	N	134	'n	26.	25	35
_	Q653u4	Q653U4	N	678	4	57.	52.5	34
lymantria d	Oxmx6O	Q9YMX0	N	1029	9	57.	53	33
ciona savig		015999	7	741	9	57.	53	32

# ALIGNMENTS

RESULY 1  PR39_PIG  D1

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RESULT 3
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22255705; PubMed=1236864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
neutrophils that is analogous to PR-39, an antibacterial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
          the small intestine.";
J. Leukoc. Biol. 56:807-811(1994).
-!-FUNCITON: Exerts a potent antimicrobial activity against both E.coli and B.megaterium.
-!- TISSUE SPECIFICITY: Small intestine and bone marrow.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
Proline amide (G-170 provides amide
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081LQ0;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Spliceosome-associated protein, putative.
ORFNames-PF14 0194;
Plasmodium falciparum (isolate 3D7).
Elasmodium falciparum (isolate 3D7).
                                                                                                                                                                                                                                                                                                                                                                            Antibacterial protein PR-39.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 92; DB 1; Length 172;
; Pred. No. 0.0003;
0; Mismatches 0; Indels
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G -> A (in Ref. 1).

A -> T (in Ref. 1).

RQ -> QR (in Ref. 1).

IMS -> NDP (in Ref. 1).

P -> I (in Ref. 5).

W, 994B792798COB133 CRC64;
                                                                                                                                                                                           EMBL, X87236; CAA60682.1; -.
EMBL, X87236; CAA61487.1; -.
EMBL, X89221; CAA61487.1; -.
EMBL, SA232; SA232; SA232;
HSSP, P32136; IKWI.
R PROSTON; PRO01894; Cathelicidin.
R ProDom; P0001898; Cathelicidins; 1.
R PROSTE; PS00946; CATHELICIDINS_1; R PROSTE; PS00947; CATHELICIDINS_2; 1.
W Amidation; Antibiotic; Direct protein sequencing; W Amidation; Antibiotic; Direct protein
R Pyrrolidone carboxylic acid; Signal.
SIGNAL 1
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157 157 F
172 AA; 19476 MW;
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Best Local Similarity 100.
Matches 15; Conservative
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169
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124
169
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107
169
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CONFLICT
SEQUENCE
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Nature 419:512-519(2002).

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/ABLO1000316; EAA20492.1; -.

HSSP; P11940; ICWJ.

InterPro; IPR000564; RNA_rec_mot.

Pfam; PF00076; RRM; 2.

PROSITE; PSS0102; RRM; 2.

SRQUENCE 415 AA; 46441 MW; 6D9D28AF80357B0A CRC64;
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Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Roo P.W., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Sull J.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.5%; Score 63; DB 2; Length 415; 76.9%; Pred. No. 3.4; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.8%; Score 67; DB 2; Length 484; Best Local Similarity 76.9%; Pred. No. 1.3; Matches 10; Conservative 0; Mismatches 3; Indels
                                                                                                                            "Genome sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                           EMBL; AE014819; AAN36806.1; -.
HSSP; P11940; LTVJ.
TITLE-PPO; 1PR.000504; RNA_rec_mot.
Pfam; PF00076; RRM_1; 2.
SWART; SM0360; RRM; 2.
SEQUENCE PSSO102; RRM; 2.
SEQUENCE 484 AA; 53722 NW; 0858953D48F72E2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                    Nature 419:498-511 (2002)
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InterPro; IPR010916; PLAT_LH2.
InterPro; IPR010916; TONB_Box_N.
Pfam. PF06232; ATS3; 1.
PROSITE; PS00430; TONB_DEPENDENT REC 1; UNKNOWN 1.
SEQUENCE 213 A4; 23\(\tilde{0}\)99 MW; DE74E\(\tilde{0}\)40.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AR370461; AAL47396.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
105-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Landsberg erecta;
MEDLINE=99308509; PubMed=10380802; DOI=10.1023/A:1006101404867;
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Pred. No. 9.4;
0; Mismatches 4; Indels
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InterPro; IPR008976; PLAT_LH2.
InterPro; IPR010916; TONB_Box_N.
Pfam; PF06232; ATS3; 1.
PROSITE; PS00430; ATS3; DEPENDENT REC 1; UNKNOWN 1.
SEQUENCE 213 AA; 23\overline{05}57 MW; D\overline{05}745727EDF9B34 CRC64;
                                                                                           Last sequence update)
Last annotation update)
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                              PRT;
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EMBL; AF067858; AAC27073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.0%;
69.2%;
                                                                   01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26, Embryo-specific protein 3.
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Best Local Similarity 6>...
Best Local 9; Conservative
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                              PRELIMINARY;
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             081271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
BEVAN M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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               Score 57; DB 2; Length 213;
Pred. No. 9.4;
0; Mismatches 4; Indels
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STRAIN=WS576;
MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; All63652; CAB87275.1;
PIR; T48490; T48490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PÉAN; PF06232; ATS3; 1.
PROSITE; PS00430; TONB DEPENDENT REC 1; UNKNOWN 1.
SEQUENCE 213 AA; 23083 MW; DE6230ACB1172834 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Embryo-specific protein 3 (ATS3).
Name-T2814 130;
Arabidopsis-thaliana (Mouse-ear cress).
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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69.2%; Pred. No. 9.4;
tive 0; Mismatches
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InterPro; IPR008976; PLAT_LH2.
InterPro; IPR010916; TONB_Box_N.
                      62.0%;
69.2%;
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Query Match
Best Local Similarity 69.4.
Local 9; Conservative
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Matches 9; Conservative
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nes 10; Conservative
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Q624P0;
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WNK1_HUMAN
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MEDLINE-98367519; Pubmed=9692967; DOI=10.1021/bi9808013;
Zhang Y., Brown R.D. Jr., West C.M.;
"Two proteins of the Dictyostelium spore coat bind to cellulose in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PÓ530H05.25).
Name-OSJNBA0023122.10; Synonyms=P0530H05.25;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
"Two proteins of the Dictyostelium spore coat bind to cellulose in
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Saeski T., Matsumoto T., Yamamoto K.;
"Cryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC clone:OS/NBa00221322.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0023122.10 (Hypothetical protein
                                                                                                                                                                          Score 56; DB 2; Length 135;
Pred. No. 7.7;
3; Mismatches 3; Indels
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Pred. No. 8;
3; Mismatches 3; Indels
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                                                                                                                                        135 AA; 14829 MW; 500634A988A49408 CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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(TrEMBLrel. 28, Last sequer (TrEMBLrel. 28, Last anno
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EMBL, AF066073; AAC19125.1; -.
DictyBase; DDB0185060; pspB.
                                   Biochemistry 37:10766-10779(1998)
EMBL, AF066072; AAC19124.1; -.
DictyBase; DDB0185060; pspB.
                                                                                                                                                                              60.9%;
53.8%;
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53.8%;
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Best Local Similarity 53.87
Conservative
7;
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Best Local Similarity 53.8
Matches 7; Conservative
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SEQÜENCE
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SEQUENCE
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Q67VV4
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LOCATION.
TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein OSJNBa0060017.6.

Name=OSJNBa0060017.6;
Oryza sativa (japonica cultivar-group).

Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryza.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                   SEGUENCE FROM N.A.
Saaski T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
"Orne:P0510H05.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OSJNBa0060017.";
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                   EMBL, AP004733; BAD37715.1; -.
EMBL, AP00541; BAD37390.1; -.
Hypothetical protein.
SEQUENCE 150 AA; 16041 MW; 2C1B2FB6B092D311 CRC64;
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Last annotation update)
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Name=PRKWNK1; Synonyms=KDP, KIAA0344;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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MEDLINE=22388257; Pubhed=12477912; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Alausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carnhord P., Frange C.,
RA Stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smallus D.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smallus D.E.,
Rodriguez C., Grimwood J., Schmutz J., Marra M.A.;
Rodriguez C., Grimwood J., Schmutz J., Marra M.A.;
Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;
Rodriguez C., Grimwood J., Schmutz J., Marra M.A.;
Rodriguez M., Rrzzywinski M.I., Skalska U., Smallus D.E.,
Rodriguez C., Grimwood J., Schmutz J., Marra M.A.;
Rodriguez M., Rrzzywinski J., Marra M.A.;
Rodriguez M., Rrzzywinski J., Marra M.A.;
Rodriguez M., Rrzzywinski J., Marra M.A.;
Rodriguez M., Rrzzywinski J., Rrzzywinski J., Marra M.A.;
Rodriguez M., Rrzzywinski J., Marra M.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21390047; PubMed=11498583; DOI=10.1126/science.1062844; Wilson P.H., Disse-Nicodeme S., Choate K.A., Ishikawa K., Nelson-Williams C., Desitter I., Gunel M., Milford D.V., Lipkin G.W., Achard J.M., Feely M.P., Dussol B., Berland Y., Unwin R.J., Mayan H., Simon D.B., Farfel Z., Jeunemaitre X., Lifton R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morris J.D.H.;
"PSK, a novel STE20-like kinase derived from prostatic carcinoma that
activates the JNK MAPK pathway and regulates actin cytoskeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22158633; PubMed-12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
Construction of expression-ready cDNA clones for KIAA genes: manual
curation of 330 KIAA cDNA clones.";
                                                                                                                                                                                                                                                                                  Corvol P., Jeunemaitre X.; "Multiple promoters in the WNK1 gene: one controls expression of kidney-specific kinase-defective isoform."; Mol. Cell. Biol. 23:9208-9221(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-670 FROM N.A. (ISOFORM 1/2), FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                Verissimo F., Jordan P.; "WRK kinases, a novel protein kinase subfamily in multi-cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Breast carcinoma;
MEDLINE-20127920; PubMed=10660600; DOI=10.1074/jbc.275.6.4311;
MODITO T.M., Garg R., Johnson C., Coptcoat M.J., Ridley A.J.,
MEDLINE=21455683; PubMed=11571656; DOI=10.1038/sj/onc/1204726;
                                                                                                                                                                                                                                                    Delaloy C., Lu J., Houot A.M., Disse-Nicodeme S., Gasc J.M.,
                                                                                                                                                                                                  TISSUE=Kidney;
PubMed=14645531; DOI=10.1128/MCB.23.24.9208-9221.2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 69-2382 FROM N.A. (ISOFORM 2).
                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 275:4311-4322(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 3)
                                                                                                                Oncogene 20:5562-5569(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 4:141-150(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organisation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
                                                                                           organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch). Isola-0944A3-3; Sequence=VSP 050635, VSP 050636;
Name=4; Synonyms=Kidney-specific, Kinase-defective;
Isola-0944A3-4; Sequence=VSP 050634, VSP 050637;
TISSUE SPECIFICITY: Widely expressed, with highest levels observed in the testis, heart, kidney and skeletal muscle.
DISEASE: Defects in PRKWNK1 are a cause of pseudohypoaldosteronism type II (PHAII) [MIM:145260]. PHAII is an autosomal dominant. disease characterized by severe hyportension, hyperkalemia, and sensitivity to thiazide diuretics which may result from a chloride shunt in the renal distal nephron.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. WNK õ -!- CAUTION: Cys-250 is present instead of the conserved Lys which is expected to be an active site residue. Lys-233 appears to fulfill Event=Alternative promoter; Comment=2 isoforms, 1 (shown here) and 4, are produced by use GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005524; F:ATP binding; IDA.
GO; GO:0004524; F:ATP binding; IDA.
GO; GO:0004681; F:protein serine; ISS.
GO; GO:000743; P:protein amino acid phosphorylation; IDA.
GO; GO:000743; P:protein maino acid phosphorylation; IDA.
GO; GO:000743; P:protein kinase cascade; IDA.
GO; GO:005049; P:regulation of callular process; ISS.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr\_pkin\_AS.
PF00069; Pkinase; IBOId=09H4A3-2; Sequence=VSP\_050638;
Note=No experimental confirmation available; Event=Alternative splicing; Named isoforms=4; Probom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE\_ST; 1. IsoId=09H4A3-1; Sequence=Displayed; the required catalytic function. EMBL, AJ296290, CACISO59.1; -EMBL, AY21477; AA046160.1; -EMBL, BC021121, AA421121.1; -EMBL, AF061944; AA731483.1; -EMBL, AF0612942; BAA20802.2; -Genew, HGNC.14540; PRKWNK1.
MIM, 605232; -MIM; 145260; -alternative promoters; Name=1 ---÷ 

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Q8N1K8
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1 394 2382 /FTIGHTGATE - FINEXTISTA (III IEDICALII III)
1 408 437 FORMALEMATERYPESCONAQIYRRYTS -> MDIKKKD FCSVFVIINSHCCCCPQKDCINE (III ISOFORM 4).
1 792 1037 Missing (III Ref. 4).
1 792 1037 Missing (III Ref. 4).
1 794 670 VS -> GG (III Ref. 4).
1 740 Missing (III Ref. 5).
1 1806 1808 I - M (III Ref. 5).
1 1836 1836 Missing (III Ref. 5).
2 2382 AA; 250755 WW, ADDAGC86554B7FCA CRC64;
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Alternative promoter usage; Alternative splicing; ATP-binding; Phosphorylation; Protein kinase inhibitor; Serine/threonine-protein kinase; Transferase.

DOMAIN 221 479 ATP (By similarity).

NP BIND 227 235 ATP (By similarity).

ACT SITE 349 349 Protein (By similarity).

ACT SITE 378 378 Phosphoserine (by autocatalysis) (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                               similarity).
Phosphoserine (by autocatalysis) (By
                                                                                                                                                                                similarity).
Misaing (in isoform 4).
FTIG=VSP 050634.
TPEFMAPE => MFQVYLGA (in isoform 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0005525; F:GTP binding; IEA.
GO; GO:0003924; F:GTPase activity; IEA.
InterPro; IPR00130; GED.
InterPro; IPR00130; GED.
InterPro; IPR01849; PH.
InterPro; IPR01849; PH.
Ffan; PF01031; Dynamin_M; 1.
Pfam; PF02212; GED; 1.
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72.7%;
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nes 8; Conservative
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                                                                                                                                                               382
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                                                                                                                                                                                                                                    393
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                                                                                                                                                                                                                                    386
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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Q9UPHS
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Pubmed=14702039; DOI=10.1038/ng1285; Pubmed=14702039; DOI=10.1038/ng1285; Pubmed=14702039; DOI=10.1038/ng1285; Pubmed=14702039; DOI=10.1038/ng1285; Pubmed=14702039; DOI=10.1038/ng1285; Pubmed=14702039; DOI=10.1038/ng1285; Pubmed=14702039; Pubmed=14702039; Pubmed=14. Suckit Y., Nakamus Y., Makhara Y., Magharan Y., Magharan Y., Magharan Y., Magharan Y., Magharan Y., Ramanoto J., Sailor H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Rahahashi M., Kanda K., Yokoi T., Furuya T., Kikawa B., Omra Y., Rahahashi M., Katsuta N., Sato K., Tanikawa B., Omra Y., Rahahashi M., Kantanabe M., Hiraoka S., Chiba Y., Ishidas S., Ranai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kusano J., Ranai H., Kimata M., Watanabe S., Yosida M., Imose N., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Ranashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Nomiyama H., Sach N., Takami S., Terashima Y., Wakadawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Ranazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okmaru Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamura X., Matsumura X., Mata H., Watanabe M., Komatsu T., Sugano S., Matsuhama R., Sasaki M., Takahashi Y., Nakajawa Y., Matauna Y., Matanabe M., Komatsu T., Sagaki M., Atau H., Watanabe M., Komatsu T., Shigase T., Nomura Y., Nomura Y., Nakamura Y., Nakamura Y., Nakamura Y., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai R., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai R., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai R., Yada T., Nakamura Y., Ohara O., Isogai T., Sagani R., Nakai R., Sagani R., Sagani R., Sagani R., Sagani R., Sagani R
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                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein FLJ40556.
Homo saplans (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                              Length 393;
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SMART; SM00302; GED; 1. SMART; SM00233; PH; 1. PROSITIF; PSS0003; PH_DOMAIN; 1. NON TER 1 SEQUENCE 393 AA; 44036 MW; FAA7B8456023E2D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                     Query Match 59.8%; Score 55; DB 2; Best Local Similarity 66.7%; Pred. No. 32; Matches 10; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 AA
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-!- SMILARITY: Contains 1 PH domain.
EMBL; AK097875; BAC05190.1; --
HSSP; Q05193; 2DYN.
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GO; GO:0003924; F:GTPase activity; If
InterPro; IPR000375; Dynamin_central.
InterPro; IPR003130; GED.
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Pfam; PF01031; Dynamin M; 1.
Pfam; PF02212; GED; 1.
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By Subbace From N.A.

Crimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Tran-Gyamfi M., Lamerdin J.B., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., Lamerdin J.B., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E., Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Caenepeel S., Flowers D., Fotopulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T., Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H., Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Slazak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustazzewska A., Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustazzewska A., Purey T.S., DeJong P., Dickson M., Gordon D., Eichler B.E., Pitlar B.E., Pitlar B.E., Myers R.W., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruslina K., Parmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., W.
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=96011652; PubMed=7590285; DOI=10.1016/0378-1119(95)00275-B;
Diatloff-Ziro C., Gordon A.J.E., Duchaud E., Merlin G.;
"Isolation of an ubiquitously expressed cDNA encoding human dynamin II, a member of the large GTP-binding protein family.";
Gene 163:301-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                       Query Match 59.8%; Score 55; DB 2; Length 464; Best Local Similarity 66.7%; Pred. No. 39; Matches 10; Conservative 0; Mismatches 5; Indels
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                                           PROSITE; PS50003; PH DOMAIN; 1.
SEQUENCE 464 AA; 52198 MW; A56592DDAD9B7368 CRC64;
                                                                                                                                                                                                                                                               DYNZ HUMAN STANDARD; PRT; 870 AA. P50570; Q7ZSZS; Q9UPH4; 0.0CT-1996 (Rel. 34, Crated) 05-JUL-2004 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Dynamin 2 (EC 3.6.5.5).
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                                                                                                                                                                                  431 RippGippGvpskRP 445
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                SMART; SM00302; GED; 1.
SMART; SM00233; PH; 1.
   Pfam; PF00169; PH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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DYN2_HUMAN
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Physy J. Relton B., Nettensin M., Madan A., Rolligues S., Sanchez A., Maillag M. Wadan A., Young A.C.; Shawchento Y.; Bouffact G.G.; A. Marking M. A.C.; Grimwood J., Schauct J. Myers R.M., Schariber A.C.; Grimwood J., Schauct J. Myers R.M., Schariber A.C.; Grimwood J., Schauct J. Myers R.M., Schariber A.C.; Grimwood J., Schauct J. Myers R.M., Schariber D. E., Schariber D. S., Schariber A. Schariber J. S., Marking M. S., Marking M. M. Schariber D. E., Schariber D. S., Schariber D. Schariber D. Schariber D. Schariber D. Schariber D. Schariber D. Schariber D. S.,

Job time : 53.9545 secs

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Galagan J. B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., Fitzhugh W., Man L.J., Smirnov S., Purcell S., Rehman B., Blkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endels R., Mang S., Nielsen C.B., Butler J., Endels R., As and M., Mashburne M., Rahal M., Mang S., Nielsen C.B., Batler A., Schulte U., Rothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Ramal M., Kamvysselis M., Maucell E., Beleke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Matzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., Aramayo R., Narvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Natvig D.O. (2003).

C. C. Gals M. S., Lander E.S., Nusbaum C., Birren B.; Nature O:O (2003).

C. Catcheside B., Sellam M.S., Lander E.S., Nusbaum C., Birren B.;

Nature O:O (2003).

C. Catcheside B., Markillametous Fungus Neurospora crassa.";

Nature O:O (2003).

EMBL, Genbank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, Assux1000002; EAA36403.1; -.
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.

GO; GO:0006248; F:pre-mRNA splicing factor activity; IEA.

GO; GO:0006397; P:nRNA processing; IEA.

InterPro; IPR010920; Sm_like_riboprot.

InterPro; IPR00649; snRNP.

InterPro; IPR00163; snRNP.Sm.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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45.8%; Pred. No. 19;
tive 0; Mismatches 2; Indels 11
                                                                                                                                                                   59.8%; Score 55; DB 1; Length 870;
66.7%; Pred. No. 76;
tive 0; Mismatches 5; Indels
   QI -> RV (in Ref. 1).

N -> I (in Ref. 1).

R -> P (in Ref. 1).

; 2F4567B75980935D CRC64;
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SEQUENCE 213 Aa; 21440 MW; 17356AF1B36F2240 CRC64;
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Last annotation update)
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   155 156 QI
316 316 N
324 324 R
870 AA; 98063 MW;
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nes 10; Conserv
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CONFLICT
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Best Local
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Q7SHV3
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Search completed: October 26, 2005, 05:18:37

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TOPOLOGY:
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                                                                                October 26, 2005, 05:02:04; Search time 15.4091 Seconds (without alignments) 72.667 Million cell updates/sec
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Sequence 58,
Sequence 42,
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Sequence 2, 1
Sequence 60,
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Sequence 5,
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-728-333-1
US-08-930-777A-1
PCT-US95-12080-1
US-09-739-555-1
US-08-487-359-5
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US-08-222-798A-5
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US-08-930-777A-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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92
1 RIPPGFPPRFPPRF 15
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Maximum DB seg length: 2000000000
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Match Length DB
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                                                                                                                                                                        Sequence:
                                                                                     Run on:
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Sequence 26, Appl Sequence 10, Appl Sequence 56, Appl Sequence 37, Appl Sequence 36, Appl Sequence 20, Appl Sequence 20, Appl Sequence 8, Appl Sequence 18, Appl Sequence 34, Appl Sequence 27, Appl Sequence 28, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 27, Appl Sequence 18, Appl Sequence 18, Appl Sequence 27, Appl	
US-09-854-856-26 US-09-854-856-10 US-09-854-856-56 US-09-854-856-52 US-09-854-856-52 US-09-854-856-36 US-09-854-856-36 US-09-854-856-36 US-09-854-856-34 US-09-854-856-34 US-09-854-856-34 US-09-854-856-34 US-09-854-856-34 US-09-854-856-34 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18 US-09-854-856-18	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6	
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9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

### ALIGNMENTS

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USEGULTA.

US.-08-30-777A-6

SEQUENCE 6, Application US/08930777A

SEQUENCE 6, Application US/08930777A

SEQUENCE 6, Application US/08930777A

PAPLICANT: Bit. 138 h. 138
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y Match 100.0%; Score 92; DB 1; Length 39; Local Similarity 100.0%; Pred. No. 3.3e-05; hes 15; Conservative 0; Mismatches 0; Indels
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                                                                                                          COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PatentIn Felease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,722
FILING DATE: 22-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 34,444)-815-6508
TELEPAN: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Allost
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Patent No. 5830993
GENERAL INFORMATION:
APPLICANT: Bhi, Jishu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins, Hovey, Williams, Timm
ADDRESSEE: Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Jornvall, Hans
TITLE: No. 5654273el Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RIPPGFPPRFPPRFP 15
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Boman, Hans G.
Mutt, Viktor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO PUBLICATION INFORMATION:
                                                                                       30309-4530
                                Georgia
: USA
Atlanta
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AUTHORS:
AUTHORS:
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Matches
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APPLICANT: Gallo, Richard L.
APPLICANT: Klagsbrun, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 39;
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                                                                                                                                       Sequence 1, Application US/08162052
Patent No. 5489575
GENERAL INFORMATION:
APPLICANT: LEE, Jong-Youn
APPLICANT: BOMAN, Hans G
APPLICANT: MUTT, Viktor
APPLICANT: JONENYALL, Hans
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: D. Box 1404
CITY: Alexandria
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIB: 22313-1404
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 02-UN-1994
PLIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: WO 92-22578
FILING DATE: 13-DEC-1992
ATTONEY/AGENT INPORMATION:
AMADIA: CARACLE CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL C
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Pred. No. 3.3e-05;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 00330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; SC
100.0%; Pr
tive 0;
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Patent No. 5654273
1 RIPPGFPPRFPPRFP 15
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-162-052-1
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                                                                                                                          US-08-162-052-1
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APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: BLECHA, FRANK
APPLICANT: BLICHA, FRANK
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
CLEINS MOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 92; DB 3; Length 39; 100.0%; Pred. No. 3.3e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                 Length 39;
                                                                                                                                                                                                                                            IndelB
                                                            : Jornvall, Hans
No. 5863897el Polypeptides And Their Use
: PCT WO 92/22578
                                                                                                                      DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/024,975 FILING DATE:
                                                                                                                                                                                                   Score 92; DB 2; 1
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDAER:
APPLICATION UNDAER:
APTILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 6133233
                                                                                                                                                                                                   Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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LENGTH: 39 amino acids
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-09-024-975-1
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COUNTRY: U
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AUTHORS:
AUTHORS:
AUTHORS:
AUTHORS:
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                                                                                                    JOURNAL:
                                                                                                                                                              US-08-728-333-1
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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APPLICANT: Klagsbrun, Michael

TITLE OF INVENTION:

APPLICANT: Klagsbrun, Michael

TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair

NUMBER OF SECURNICE: 1

CORRESPONDENCE ADDRESS:

ADDRESSE: Patrea L. Pabst

STREET: 1100 Peachtree Street, Suite 2800

CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 39;
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CONTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BENCOMPATIBLE
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/728,333
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INPORMATION:
NAME: Pabet, Patrea L,
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB 2; 1
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 92; DB Best Local Similarity 100.0%; Pred. No. 3.3 Matches 15; Conservative 0; Mismatches
                   ATTORNEY AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 2562
REPERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPRA: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08728333
Patent No. 5863897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RIPPGFPPRFPPRFP 15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                       single
      CLASSIFICATION: 530
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3Y: linear
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TYPE: amino acid
STRANDEDNESS: Bil
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PROPHENINS-ANTIBIOTIC PEPTIDES
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                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Dee, Jong-Youn
AUTHORS: Mutt, Viktor
AUTHORS: Jornvall, Hans
TITLE: Novel Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
                                        APPLICATION NUMBER: PCT/US95/12080
APPLICATION Nu...
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION:
TELEPHONE: (404)-815-8794
TELEFAX: (404)-815-8795
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TYPE: amino acid
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Best Local Similarity 93.3%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic US-09-739-535-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 RIPP-PPREPPRFP 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE: 12/23/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-12080-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Sequence 1. Application PC/TUS9512080

GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporaton
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1200 One Atlantic Center
STREET: 1201 West Peachtree
CITY: Atlanta
STATES: Georgia
CONTYRY: USA
ZIP: 30309-3450
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
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COMPUTER: DASS/MS-DOS
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COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
COMPUTER: DASS/MS-DOS
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100.0%; Pred. No. 3.3e-05;
tive 0; Mismatches 0; Indels
                             US-08-930-777A-1

Sequence 1, Application US/08930777A

Patent No. 6713605

GENERAL INFORMATION:

APPLICANT: Shi, Jishu

TITLE OF INFORMERS:

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

CONNTRY: Wissouri

CONNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 CALP: 04108
CAPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION STAIN PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION NUMBER: 23625-A
REPERANCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRHONE: (816) 474-9050
TELEFRAX: (816) 474-9050
TELEFRAX: (816) 474-9050
TELEFRAX: (816) 474-9050
TELEFRAX: (816) A74-9050
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-930-777A-1
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-12080-1
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Gaps
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Sequence 1, Application US/09739535

Sequence 1, Application US/09739535

Sequence 1, Application US/09739535

GENERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
APPLICANT: Cubist Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL LIFOPEPTIDES AS ANTIBACTERIAL AGENTS
FILE REFERENCE: C060.
CURRENT APPLICATION NUMBER: US/09/739,535

CURRENT FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 1

SOFUMARE: Patentin version 3.1

SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75.5; DB 4; Length 38; Pred. No. 0.0035; 0; Mismatches 0; Indels
Length 39;
                                                Indels
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; Sequence 5, Application US/08487359
; Patent No. 5633229
; GENERAL INFORMATION:
; APPLICANT: KOKRYAKOV, VLADMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: LEHRER, ROBERT I.
; TITLE OF INVENTION: PROPHENINS-ANT:
; NUMBER OF SEQUENCES: 9
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Gape
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; Sequence 3, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
    APPLICANT: BLECHA, FRANK
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
    COLLINS
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                   Length 78;
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                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP Compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.0%; Score 57; DB 76.9%; Pred. No. 0.3;
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEBHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLING, JOHN M.
REGISTRATION NUMBER: 25,262
REFERENCE/DOCKET NUMBER: 25,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
                                                                                                                                                                                                                                                                                                        62.5%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    3 PPGFP-PRFPPRFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                               34 PPQFPGPRFPPFP 47
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Best Local Similarity 78.61
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 16 amino acids
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-024-975-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Pred. No. 1.2;
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Sequence 5, Application US/08222798A

GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STRRET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
COUNTRY: USA
ZIP: 20006-1812
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING PATE: 05-APR-1994
FILING PATE: 05-APR-1994
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTONEY/AGENT INFORMATION:
NAME: MURACHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REBERENCE/DOCKET UNBER: 29,959
REBERENCE/DOCKET UNBER: 20,053.00
TELEPAN: (202) 887-1500
TELEPAN: (202) 887-1500
TELEFAN: (202) 887-1500
TELEFAN: (202) 887-1500
TELEFAN: CARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                               ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%;
78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                  STATE: CA
COUNTRY: USA
ZIP: 20006-1812
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US-08-222-798A-5
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0; Mismatches
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ATTORNEY/AGENY INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/POCKET NUMBER: 2362
TELECOMMUNICATION:
TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.0%;
Best Local Similarity 76.9%;
Matches 10; Conservative
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: peptide

US-08-930-777A-3
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STRANDEDNESS: si
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us-us-ysu-///A-b

Sequence 5, Application US/08930777A

Patent No. 6713605

GENERAL INFORMATION:

PAPLICANT: Blecha, Frank
APPLICANT: Adologous
CITY: Kanasa City
STATE: Missouri
CONNTRX: US.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPDY/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENTING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENTION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: April 10, 1996
CLASSIFICATION: 530
PRIOR APPLICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELEPHONE: (816) 474-9050
INPORMATION INPORMATION:
TELEPHONE: (816) 474-9057
INPORMATION PATA:
TELEPHONE: GROUD NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 main on acids
TVDE. A THIS AND AND A THE CALL AND A THE CONTROL AND A THE CALL AND A THE CONTROL AND A THE CONTROL AND A THE COMPUTENTION INPORMATION:
NAME: COLING, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELEPHONE: (816) 474-9057
INPORMATION INPORMATION:
TELEPHONE: HEAD AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND A THE COMPUTENT AND
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Pred. No. 0.3;
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; Sequence 3, Application US/08930777A
; Sequence 3, Application US/08930777A
; Patent No. 6710-778-7
; GENERAL INFORMATION:
    APPLICANT: Shi Jishu
; TITLE OF INFORMICES:
    NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Hovey, Williams, Timmons & Collins
    STREET: 2405 Grand Blvd., Ste. 400
    CITY: Kansas City
    STATE: Missouri
    CONNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.0%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RIPPGFPPRFPPR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide
US-08-930-777A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
GY: linear
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hovey, Williams, Timmons
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US-08-419-066-2
i Sequence 2, Application US/08419066
i Ratent No. 5830933
i GENERAL INFORMATION:
APPLICANT: Blecha, Frank
ITILE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ochin M. Collins, Hovey, Williams, Timmons
ADDRESSEE: Collins
STREET: 405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ISOUTHER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/419,066
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: 530
ATTONENTYAGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
TELEPRAK: (816) 474-9050
TELEPRAK: (816) 474-9050
TELEPRAK: (816) 474-9050
TELEPRAK: (816) 474-9050
TELEPRAK: (816) 474-9050
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TELEPRAK: (816) 474-9050
TELEPRAK: (816) 474-9050
TELEPRAK: (816) 474-9050
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Query Match
Best Local Similarity 76.9%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 3; Indels
; TOPOLOGY: linear
; MVECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2
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0; Gaps

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Search completed: October 26, 2005, 05:21:59 Job time : 16.4091 secs

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                                                                                                                                           October 26, 2005, 05:05:05; Search time 55.3636 Seconds (without alignments) 113.119 Million cell updates/sec
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Sequence 18, Sequence 14, Sequence 44, Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
Sequence 2,
Sequence 6,
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NEOS6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USOP_PUBCOMB.pep:*
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: /cqn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:'
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-651-147-6
US-10-014-147-1
US-10-31-155-1
US-10-31-155-2
US-10-31-155-6
US-10-344-709C-18
US-10-91-185-14
US-10-91-185-14
US-10-91-185-14
US-11-004-379-20
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                                                                                                                                                                                                                                                                                                                                                                                                                            1862994 segs, 417510619 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                       Sequence:
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No.
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Sequence 1, Appli Sequence 28892, Sequence 28802, Sequence 208016, Sequence 32276, Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 13302, Sequence 18350, A	Sequence 319541, sequence 2, Appli Sequence 230, Appli Sequence 230, Appli Sequence 1404, Appli Sequence 1185600, Sequence 118176, Sequence 1230243, Sequence 43436, Appli Sequence 13512, Sequence 115312, Sequence 15513,
9-738-738-738-738-738-738-738-738-738-738	-10 - 425 - 115 - 3 -10 - 105 - 938 - 10 - 105 - 938 - 10 - 1038 - 472 - 2 -10 - 408 - 768 - 768 - 10 - 408 - 768 - 10 - 425 - 115 - 10 - 425 - 115 - 10 - 425 - 115 - 2 -10 - 425 - 115 - 10 - 425 - 115 - 2 -10 - 427 - 963 - 110 - 425 - 115 - 2 -10 - 427 - 963 - 110 - 427 - 963 - 1 -10 - 427 - 963 - 1
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#### ALIGNMENTS

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RESULT 1

US-10-014-147-6

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US-10-014-147-6

Publication No. US20030125249A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

ITITE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STRET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUWREY: U.S.A.

ID: 64108

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: OCCOBER: 8, 1997

FILING DATE: OCCOBER: 8, 1997

FILING DATE: ADFIL 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRANCE NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 26,262
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1 RIPPGFPPRFPPRFP 15
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TOPOLOGY: linear
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                     STATE: Missouri
                                                                         US-10-014-147-1
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                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: 4000 Frank
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kanasa City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                         Score 92; DB 14;
Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COLlins, JOHN M.
REFERENCE/DOCKET NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26,262
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-651-147-6
                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEPAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERESTICS:
LENGTH: 15 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 amino acids
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COUNTRY: U.S.A.
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les 15; Conserva
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tes 15; Conserva
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Matches
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1 RIPPGFPPRFPPRFP 15

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TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
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                                                              APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC_Compatible
COMPUTER: IBM PC_COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 92; DB 14;
100.0%; Pred. No. 0.00046;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/930,777A
PAPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (816) 474-9057 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
Sequence 1, Application US/10014147 Publication No. US20030125249A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Simons, Michael
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Gaps

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APPLICANT: Simons, Michael
APPLICANT: Simons, Mochael
Gao, Youhe
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC COMPUTER: Dell PC COMPUTER: WORSTEM: MS XP SOFTWARE: WORDPEFECT VERSION 10 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/391,155 FILING DATE: 18-Mar-2003 CILASSIFICATION: Unknown ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 39;
                                                                               Length 39;
                                                                                                                             Indels
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Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0;
                                                                                 100.0%; Score 92; DB 15;
100.0%; Pred. No. 0.00046;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-044/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Magnolia
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION:
Relective inhibition of IKBA degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

READABLE FORM:

READABLE FORM:

READIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

COMPUTER: Dell PC

OPERATING SYSTEM: MS XP

SOFTWARE: WordPerfect version 10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/391,155

FILING DATE: 18-Mar-2003

CLASSIFICATION: Unknown

ATTORNEY AGENT INFORMATION:

NAME: DAVID FYSABARET, ESG:

REGISTRATION NUMBER: 29,693

REGISTRATION NUMBER: 29,693

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 39;
                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC OPERATING SYSTEM: MS XP SOFTWARE: Worderfect version 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity 100.0%; Pred. No. 0.00046; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: DAVIG PEABMER, ESQ.
REGISTRATION NUMBER: 29, 693
REFERENCE/DOCKET NUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEBHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (978) 525-3794
W FOR SEO ID NO: 2:
                                                                                                                                                                                                            CLASSIFICATION: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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           ZIP: 01930
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Magnolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-391-155-2
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APPLICANT: Manoharan, Muthiah
APPLICANT: Reseavan, Venkitasamy
APPLICANT: Reseavan, Venkitasamy
APPLICANT: Reseaven, Venkitasamy
APPLICANT: Reseaven, Venkitasamy
APPLICANT: Reseaven, Venkitasamy
APPLICANT: Reseaven, Venkitasamy
TITLE OF INVENTION: MODIFIED iRNA AGENTS
FILE REFERENCE: 14174-091001
CURRENT APPLICATION NUMBER: US/10/916,185
CURRENT FILING DATE: 2004-08-10
PRIOR FILING DATE: 2003-04-16
PRIOR FILING DATE: 2003-04-16
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-25
PRIOR FILING DATE: 2003-04-25
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PRIOR FILING DATE: 2003-04-25
PRIOR FILING DATE: 2003-04-25
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 60/503,414
PRIOR FILING DATE: 2003-09-26
PRIOR FILING DATE: 2003-09-26
PRIOR PRIOR APPLICATION NUMBER: US 60/510,246
PRIOR PRIOR DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
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PRIOR PILING DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
                                        Gaps
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APPLICANT: Bumcrot, David
APPLICANT: Bumcrot, David
APPLICANT: Marthew J.
APPLICANT: Waraganore, Demetrius M.
APPLICANT: Vornlocher, Hans-Peter
TITLE OF INVENTION: WETHOD OF TREATING NEURODEGENERATIVE DISEASE
FILE REFERENCE: 17574-003001
CURRENT APPLICATION NUMBER: US/10/991,286A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 92; DB 17; Length 42; 100.0%; Pred. No. 0.00049; Live 0; Mismatches 0; Indels
                                        Indels
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          Pred. No. 0.00049; Mismatches 0;
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-991-286A-44; Sequence 44, Application US/10991286A; Publication No. US20050186591A1
                                                                                                                                                                                                                                                                                                 US-10-916-185-14
; Sequence 14, Application US/10916185
; Publication No. US20050107325A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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PRIOR APPLICATION NUMBER: PCT/EP01/09529
PRIOR PILING DATE: 2000-08-17
PRIOR PLING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 92; DB 15; Length 39; 100.0%; Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION: 530
                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City STATE: Missouri COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
. OTHER INFORMATION: Description of Artificial Sequence:
US-10-344-709C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGBVI INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-651-147-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/10344709C Publication No. US20040170642A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (816) 474-505,
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RIPPGFPPRFPPRFP 15
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      NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                    ZIP: 64108
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Matches 15; Conserv
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DB 16; Length 42;

100.0%; Score 92;

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TYPE: PRT ORGANISM: Artificial
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                                 JS-09-738-742-1
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LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
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Sequence 20, Application US/11004379

Publication No. US20050153337A1

GENERAL INFORMATION:

APPLICANT:
MANDARIAN,
FILE REPERENCE: 14174-067001

CURRENT APPLICATION NUMBER: US/11/004,379

CURRENT APPLICATION NUMBER: US/410586

PRIOR PILING DATE: 2004-04-05

PRIOR PILING DATE: 2003-04-05

PRIOR PILING DATE: 2003-04-10

PRIOR PILING D
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100.0%; Score 92; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Exemplary Cell Permeation Peptide US-10-991-286A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 92; DB 18;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US2004/18271
PRIOR FILING DATE: 2004-06-09
PRIOR PILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RIPPGFPPRFPPRFP 15
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US-11-004-379-20
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Sequence 258982, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09739535
; Publication No. US20020058785A1
; GENERAL INFORMATION:
; APPLICANT: CUIDANT: SOCULATION NUMBER: US/09/739,535
; CUIDANT FILING DATE: 2000-12-15
; SOFTWARE: Patentin version 3.1
Sequence 1, Application US/09738742
Publication No. US20020025924A1
GENERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
TITLE OF INVENTION:
NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
FILE REFERENCE: C060
CURRENT APPLICATION NUMBER: US/09/738,742
CURRENT FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
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Best Local Similarity 93.3%; Pred. No. 0.039;
Matches 14; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.039;
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93.3%;
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Best Local Similarity 93.3*
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Sequence 211799, Application US/10424599
Sequence 211799, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 211799
SEQ ID NO 211799
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                                                                                                                                                                   Query Match 65.2%; Score 60; DB 15; Length 103; Best Local Similarity 66.7%; Pred. No. 6.3; Matches 10; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_33281C.1.pep
US-10-424-599-211799
                                                                                 FEATURE:

COTHER INFORMATION: Clone ID: PAT_MRT3847_75885C.1.pep

US-10-424-599-258982
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                  LENGTH: 103
TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-211799
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October 26, 2005, 04:51:43; Search time 55:1091 Seconds (without alignments) 98.253 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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83
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Perfect
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:\*geneseqp2003bs:\*geneseqp2004s:\* A\_Geneseq\_16Dec04:\* L: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2000s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	. uo	Leukocyte	Proline/A	Proline-a	Antimicro	PR-39 der	PR-39 der	Amino aci	Leukocyte	Proline-a	Antimicro	Leukocyte	Proline/A	Proline-a	Antimicro	Antibacte	Magainin-	Synducin	Leukocyte	Proline/A	PR-39 pep	PR-39 pep	Amino aci	Antimicro	Proline-a	Antimicro
	Description	Aaw01450	Aaw75725	Ade86118	Ad167260	Aab26885	Aab97277	Aab84691	Aaw01452	Ade86115	Ad167257	Aaw01447	Aaw75723	Ade86113	Ad167255	Aar30491	Aar99121	Aar94446	Aaw01446	Aaw75722	Aab26888	Aab97280	Aab84690	Add35364	Ade86112	Ad167254
SUMMARIES	QΙ	AAW01450	AAW75725	ADE86118	ADL67260	AAB26885	AAB97277	AAB84691	AAW01452	ADE86115	ADL67257	AAW01447	AAW75723	ADE86113	ADL67255	AAR30491 .	AAR99121	AAR94446	AAW01446	AAW75722	AAB26888	AAB97280	AAB84690	ADD35364	ADE86112	ADL67254
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	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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ABB07714 ADR82250 AAB51194 AAB1451 ADE86114 ADG67256 AAR79211 AAR79212 AAR79212 AAR79212 AAR79212 AAR79213 ABU59576 ABB07713 AAB51197 AAB51197	AAB97278 AAB84692 ABG33050 ADB87318
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## ALIGNMENTS

Inhibitor, leukocyte O2- production, proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; bunk synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; superoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy. Leukocyte O2- production inhibitor peptide PR14. AAW01450 standard; peptide; 14 AA. (first entry) 18-JUN-1997 AAW01450; AAW01450

96WO-US004674. WO9632129-A1 10-APR-1996; 17-OCT-1996. Synthetic. 

(UNIV ) UNIV KANSAS STATE RES FOUND. 95US-00419066. Shi J; 10-APR-1995;

WPI; 1996-476842/47. Blecha F,

Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39,

Claim 12; Page 28; 45pp; English.

AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. These sequences, and PR39, can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (O2-) production. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte 02-

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definition into a mammal's bloodstream reduce reperfusion injury administration into a mammal's bloodstream reduce reperfusion injury (production of reactive oxygen species, neutrophil adherence to endothelium, and extravasation of neutrophils). These peptides have two endothelium, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXP, where P is a proline residue and X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was catablished by structural and function analysis that a peptide should cleanly contain 4 or 6 of these motifs, and that inhibition. It was established with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the cutrophil superoxide anion, and also the inhibition of neutrophil chemotaxis. From this, it was found that all of the peptides inhibited NADPH oxidase to some extent. All of the peptides also inhibit neutrophil convinces and the supersected of the most potent endogenous down regulator of NADPH oxidase yet discovered, and from the data produced, it can be suggested to be involved in eliminating or reducing the reperfusion injury induced adhesion and extraction of neutrophils.
production. The peptides can be used as medicaments for fighting infection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
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                                                                                                                                                                  Length 14;
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Pred. No. 0.0012;
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                                                                                                                                                                100.0%;
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                                                                                                                                                                                    Similarity
                                                                                                                          Sequence 14 AA;
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Best Local (
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AAW75725
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The peptides are also useful in connection with surgical procedures such as coronary bypass and organ transplantation surgery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs
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                                                                                                                                                                                                                                                                                                                                                                                          Leukocyte superoxide anion; leukocyte O2- production; leukocyte attraction; proline-arginine-rich antimicrobial peptide; PR-rich antimicrobial peptide; neutrophil; wound site; infection; tissue damage; oxygen radical; antibacterial.
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                                                                             100.0%; Score 83; DB 2; Length 14; 100.0%; Pred. No. 0.0012; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                Proline-arginine (PR)-rich antimicrobial peptide PR-14.
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                                                                                                                                                                                                                                                                  ADE86118 standard; peptide; 14 AA.
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Matches 14; Conservative
                                                                                                                    14; Conservative
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                                                                                   Query Match
Best Local Similarity
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08-OCT-1997;
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Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;

myocardial ischaemia; proteasome

16-MAR-2000; 2000WO-US007050

WO200057895-A1.

Synthetic.

05-CT-2000.

99US-00276868

26-MAR-1999;

PR-39 derived angiogenesis regulatory peptide 1.

01-FEB-2001 (first entry)

AAB26885;

AAB26885 standard; peptide; 15 AA.

RESULT 5 AAB26885

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The invention relates to inhibiting leucocyte superoxide anion (02-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The activation of the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit to 126 amino acids, for a time and under conditions effective to inhibit conditions effective to inhibit conditions of the peptide inhibits the activity of Nubbh oxidase responsible for anion production, by binding to Src composite leucocyte and the mammalian leucocyte is a mammalian or conditions, where the sum of the proline and arginine residues in the proposition proline and arginine residues in the condition proline in the peptide is at least 6 or 74 % of the total number of amino acids, where the sum of the proline and arginine residues in the condition of pathphox in whole cells, therefore interfering with the binding condition and arginine residues in the peptide are arginine residues. The method of the invention is useful condition and arginine residues in the peptide are arginine residues. The method of the invention is useful condition and arginine residues in the condition and arginine residues are arginine residues. The method of the invention is useful a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leucocytes. The present condition is PR-39 analog, PR-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
                                                                                                                                                                   Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-14.
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Pred. No. 0.0012;
0; Mismatches 0; Indels
                                                                                                                                  Antimicrobial peptide PR-39 analog PR-14.
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                ADL67260 standard; peptide; 14 AA.
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                                                                                             (first entry)
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Best Local Similarity 100.
Matches 14; Conservative
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08-OCT-1997;
                                                                                             20-MAY-2004
                                                                                                                                                                                                                                                        Unidentified
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ADL67260
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This invention relates to a method for the stimulation of angiogenesis in situ within a targeted collection of viable cells. The method comprises introducing, into the cytoplasm, at least 1 member of the PR-39 oligopeptide collective, which interacts with cytoplasmic proteasomes. Part of the proteolytic activity of the proteosomes is selectively altered so as to stimulate angiogenesis. The method is used to induce angiogenesis in tissue that has suffered anoxia or infarction, e.g. myocardial infarction or chronic myocardial ischaemia, and also to study the mechanisms that control angiogenesis. The present sequence represents a PR-39 derived peptide which interacts with the proteasome and can be used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                  Stimulating angiogenesis in situ, useful e.g. for treating anoxia and infarction, by administering a PR-39 oligopeptide that regulates enzymatic activity of proteosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR-39; cathelin; inflammation; wound healing; myocardial infarction; proteasome; proteolysis; alpha7; peptide degradation; anglogenesis; anoxia; chronic myocardial ischaemia; heart tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 83; DB 3; Length 15; 100.0%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                           (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB97277 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 40; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR-39 derived peptide PR-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKKPKPPYLPKPKP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-628319/60.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                           Simons M, Gao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB97277;
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2X2X5X5X5XXXX
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Gaps ö

> 1 RRRPRPPYLPRPRP 14

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Sequence 15 AA;
                                  29-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-0CT-1996
                                                                                                                                                                     proteasomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                  Simons M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW01452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                        Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39 is a member of the the cathelin family of proteins, mature PR-39 is 39 anino acids in length (see AAB97280), and has been shown to play a role in several inflammatory events including wound healing and myocardial infarction. The PR-39 derived family of oligopeptides cause selective inhibition of proteasome mediated degeneration of peptides and stimulation of angiogenesis after their intraccilular introduction to a target cell. PR-39 derived peptides are able to interact with at least the alpha7 subunit of the proteasomes, and therefore alter the corresponding control of proteasomes such that a selective increased expression of specific proteins occurs. The invention includes methods for the selective inhibition of proteasome mediated peptide degradation. The method provides means for stimulating angiogenesis as required in living tissues and organs which have suffered defects or have undergone anoxia and/or infarction, myocardial infarction or chronic myocardial senoth muscle, artery or vein, lung, brain, kindry, spleen, liver, gastrointestinal or nerve tissues, limbs, and extremities. A particular example is after myocardial infarction or ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                        Stimulation of angiogenesis and inhibition of proteasome mediated degradation in cells, by introduction of PR-39 oligopeptide or its N-terminal fragments or their conjugates, for use in anoxia and infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
myocardial infarction; chronic myocardial ischemia; heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a PR-39 derived peptide (residues 1-15).
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                                                                                                                      (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB84691 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                        Claim 12; Page 42; 52pp; English.
                                                                     06-OCT-2000; 2000WO-US027552
                                                                                              99US-00426011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRRPRPPYLPRPRP 14
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                                                                                                                                                                     WPI; 2001-355179/37.
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                                                                                                                                              Gao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
                      WO200130368-A1.
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Unidentified
                                                                                              25-OCT-1999;
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                                                                                                                                                                                                                                 conditions.
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                                               03-MAY-2001
                                                                                                                                              Simons M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB84691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig; antimicrobial peptide; small intestine; human; neutrophil; bacteria; DNA synthesis; protein synthesis; inhibitor; syndecan expression; mesenchymal cell; wound repair; supercoxide anion; infection; leukocyte; tissue damage; oxygen radical; inflammatory disease; therapy.
                                                                                                                                                                                                                                                                                                                                   Selective inhibition of IkappaBalpha degradation within targeted viable cell collection, involves interacting PR-39 oligopeptide with IkappaBalpha and proteasomes, and altering proteolytic activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                       (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 58; 69pp; English.
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100.0%;
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27-DEC-2000; 2000WO-US035293
                                                                   99US-00474967
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                       WPI; 2001-441690/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease and anoxia
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isolated from porcine small intestine, and has also been identified in human and porcine small intestine, and has also been identified in human and porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 Kills bacteria by interfering with DNA and/or protein synthesis. PR39 also induces syndecan expression on mesenchymal cells. Syndecans are important in wound repair, showing that PR39 can be used in wound repair, as well as in antibacterial agents. These sequences, and PR39, can be used in the method of the invention is for inhibiting leukcoyte superoxide anion (O2-) production. The method comprises administering to a leukcyte a peptide (such as this sequence) capable of inhibiting leukcoyte a production. The peptides can be used as medicaments for fighting infection by attracting leukcoytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by the stating and also be used to develop products for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method of inhibiting leukocyte superoxide anion (O2-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leukocyte superoxide anion; leukocyte O2- production;
leukocyte attraction; proline-arginine-rich antimicrobial peptide;
PR-rich antimicrobial peptide; neutrophil; wound site; infection;
tissue damage; oxygen radical; antibacterial.
                                   AAW01447-W01454 represent fragments of the proline-arginine rich
                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                           Score 83; DB 2; Length 19; Pred. No. 0.0016; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proline-arginine (PR)-rich antimicrobial peptide PR-19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; SEQ ID NO 4; 24pp; English.
Disclosure; Page 27; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE86115 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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97US-00930777
                                                                                                                                                                                                                                                                                                                                                                                                                       100.001
                                                                                                                                                                                                                                                                                                                          inflammatory disease states
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Best Local Similarity luv...
Local 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blecha F, Shi J;
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                                                                                                                                                                                                                                                                                                                                                               Sequence 19 AA;
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08-OCT-1997;
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Gaps

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The invention relates to inhibiting leucocyte superoxide anion (02-)

production using a naturally occurring proline-arginine (PR)-rich
antimicrobial peptide known as PR-39 and its truncated analogs. The
cuertial comprises contacting leucocytes with the peptide comprising 39 or
comprises contacting leucocytes with the peptide comprising 39 or
comprises contacting leucocytes with the peptide comprising 39 or
complex anion acids, for a time and under conditions effective to inhibit
complex comprises responsible for anion production, by binding to Sirc
complex complex complex. The leucocyte is a mammalian or
cof the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or
cof the phagocytic and the mammalian leucocyte is neutrophil. Another
complex disclosed which employs a PR-39 analog that comprise 16
complex where the sum of the proline and arginine residues in the
complex complex complex complex of amino
complex complex complex complex complex of amino
complex complex complex colls, therefore interfering with the binding
cof p47phox to p22phox. At least 14 or 25% of the amino acid residues in
the peptide are arginine residues. The method of the invention is useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nhibiting leukocyte oxygen radical production comprises contacting a eukocyte with a peptide, where the inhibition occurs as a consequence of
attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence represents a PR-rich antimicrobial peptide.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leucocyte; superoxide anion; oxygen radical; proline-arginine; antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil; infection; wound; tissue damage; PR-39 analog; PR-19.
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                                                                                                                                                                               100.0%; Score 83; DB 8; I
100.0%; Pred. No. 0.0016;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptide PR-39 analog PR-19.
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binding between the peptide and p47phox.
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                                                                                                                                                                                                                                                                                                                                                                                                         ADL67257 standard; peptide; 19
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                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                  Local Similarity
hes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004043934-A1.
                                                                                                                                              Sequence 19 AA;
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08-OCT-1997;
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                                                                                                                                                                                    Query Match
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Gaps

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Length 26;

Score 83; DB 2; L Pred. No. 0.0021; ; Mismatches 0;

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14; Conservative 1 RRRPRPPYLPRPRP

Similarity

Query Match Best Local Matches 14

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100.0%;

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AAW01447-W01454 represent fragments of the proline-arginine rich antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first isolated from porcine small intestine, and has also been identified in human and porcine neutrophils. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis. PR39 kills bacteria by interfering with DNA and/or protein synthesis are important in wound repair, showing that mesenchymal cells. Syndecans are important in wound repair, showing that CPR39 can be used in the method of the invention. The method of the invention is for inhibiting leukocyte superoxide anion (O2-) production. The method comprises administering to a leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte a peptide (such as this sequence) capable of inhibiting leukocyte a conduction. The peptides can be used as medicaments for fighting infection by attracting leukocytes to a wound site and restricting tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. They can also be used to develop products for treating
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for inhibiting leucocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leucocytes a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leucocytes. The present sequence is PR-39 analog, PR-19.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibition of leukocyte super:oxide anion prodn. and attraction of leukocytes - using peptide(s) partic. based on antimicrobial PR-39.
                                                                                                                                                                                                        ö
                                                                                                                                                                Length 19;
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukocyte O2- production inhibitor peptide PR26.
                                                                                                                                                              Score 83; DB 8;
Pred. No. 0.0016;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                         AAW01447 standard; peptide; 26 AA.
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                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US004674.
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                                                                                                                                                                                                                                                                                     RRRPRPPYLPRPRP 14
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                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                           1 RRRPRPPYLPRPRP
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                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shi J;
                                                                                                                         Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAW01447;
                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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Sequences AAW75722-W7573 are proline/arginine rich peptides that upon administration into a mammal's bloodstream reduce reperfusion injury (production of reactive oxygen species, neutrophil adherence to endothelium, and extravasation of neutrophils). These peptides have two requirements: they contain the consensus sequence PXXP, where P is a proline residue and X is any amino acid residue, which has been found to inhibit superoxide production, and secondly they have arginine residues of inhibit superoxide production, and secondly they have arginine residues adjacent to these motifs, required for effective inhibition. It was crabilished by structural and function analysis that a peptide should indeally contain 4 or 6 of these motifs, and that inhibitory activity is correlated with the increase of length of peptides. The effectiveness of these peptides was determined by investigating the production of the correlated with the increase of length of peptides. The effectiveness of them to the section of the peptides and also the inhibition of neutrophil chemotaxis. From this, it was found that all of the peptides inhibited considered to section to a liminating or reducing considered in the reperfusion injury induced adhesion and extraction of neutrophils. The peptides are also useful in connection with surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                           Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium; superoxide, neutrophil superoxide anion; chemotaxis; NADPH oxidase; coronary bypass; organ transplantation surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reduction of reperfusion injury in temporarily occluded blood vessels by administration of a peptide which is rich in proline or arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 83; DB 2; Length 26; 100.0%; Pred. No. 0.0021; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                              Proline/Arginine rich peptide PR-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 14-15; 35pp; English
                                                                                                Æ.
                                                                                                AAW75723 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US003207
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   14
                                                                                                                                                                       (first entry)
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Matches 14; Conservative
1 RREPREPYLPRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blecha F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-495359/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                              WO9835690-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-1998;
                                                                                                                                                                       19-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-1998.
                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                     AAW75723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSS CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                             RESULT 12
                                                                                AAW7572
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Antimicrobial peptide PR-39 analog PR-26.

20-MAY-2004 (first entry)

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The present invention relates to a method of inhibiting leukocyte superoxide anion (O2-) production and/or attracting leukocytes. The method comprises the use of proline-arginine (PR)-rich antimicrobial peptides or their truncated analogues. The method is useful for attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or a neurophil, to a location, e.g. a wound site. The PR-rich peptides are useful as medicaments to fight infection by attracting leukocytes to a wound site, while restricting tissue damage at the wound site caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Attracting leukocyte to location by administering peptide including proline-arginine-rich antimicrobial peptide or its truncated analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     excessive oxygen radicals produced by these leukocytes. The present
sequence represents a PR-rich antimicrobial peptide.
                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                        Leukocyte superoxide anion; leukocyte O2- production; leukocyte attraction; proline-argánine-rich antimicrobial peptide PR-rich antimicrobial peptide, neutrophil; wound site; infection; tissue damage; oxygen rádical; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83; DB 8; Length 26;
Pred. No. 0.0021;
; Mismatches 0; Indels
                                                                                                                                                                                             Proline-arginine (PR)-rich antimicrobial peptide PR-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 2; 24pp; English.
                                                                                                     ADE86113 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00419066.
1 RRRPRPPYLPRPRP 14
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-059188/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BLEC/) BLECHA F. (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blecha F, Shi J;
                                                                                                                                                                                                                                                                                                                                       US2003125249-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-1995;
08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the location.
                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2003
                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                   ADE86113;
                                                                         RESULT 13
                                                                                    ADE86113
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The invention relates to inhibiting leucocyte superoxide anion (02-)
production using a naturally occurring proline-arginine (PR)-rich
antimicrobial peptide known as PR-39 and its truncated analogs. The
antimicrobial peptide known as PR-39 and its truncated analogs. The
antimicrobial peptide known as PR-39 and its truncated analogs. The
comprises contacting leucocytes with the peptide comprising 39 or
a senion acids, for a time and under conditions effective to inhibit
compared an anon production. The peptide inhibits the activity
compared an anonal production. The peptide inhibits the activity
compared to a NaDPH oxidase complex. The leucocyte is a mammalian or
porcine leucocyte and the mammalian leucocyte is neutrophil. Another
compared is also disclosed which employs a PR-39 analog that comprise 16
amino acids, where the sum of the proline and arginine residues in the
catids. This peptide is at least 66 or 74 % of the total number of amino
cof paptide inhibits leucocyte 0.2 production by the effective
cof paptide are arginine residues. The method of the invention is useful
cof paptide are arginine residues. The method of the invention is useful
considered as medicaments for fighting infections by attracting leucocytes to
a wound site, yet restrict tissue damage at the wound site caused by
considered the constant of the peptide are argundered the method of the invention is useful
considered to a subsetul as medicaments for fighting infections by attracting leucocytes to
a wound site, where the sum of the production. The peptides are
considered to a subsetul as medicaments for fighting infections of the method of the invention of the peptide are
considered to a subsetul as medicaments for fighting infections of the method of the invention of the peptide are
considered to a subsetul as medicaments for fighting infections of the method of the invention of the peptide are argundanced to the peptide are argundanced to the peptide are argundanced to the peptide are argundanced to the peptide are argundanced to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  excessive oxygen radicals produced by these leucocytes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                   Leucocyte; superoxide anion; oxygen radical; proline-arginine;
antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;
infection; wound; tissue damage; PR-39 analog; PR-26.
                                                                                                                                                                                                                                                                           l. .3
'notes "Essential for antibacterial activity"
                                                                                                                                                                                                                                                                                                               20. .26 /note= "Essential for antibacterial activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2; 24pp; English
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is PR-39 analog PR-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2003; 2003US-00651147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00419066
97US-00930777
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BLEC/) BLECHA F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blecha F, Shi J;
                                                                                                                                                                                                                                                                                                                                                                                             US2004043934-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHIJ/) SHI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-1995;
08-OCT-1997;
                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-2004
                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                           Region
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Matches
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RRRPRPPYLPRPRP 14 RRRPRPPYLPRPRP 14

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ADL67255 standard; peptide; 26 AA.

RESULT 14

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1 RRRPRPPYLPRPRP 14

RESULT 15

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This peptide was isolated from the small intestine of a pig. The small inestine is an important endocrine organ and many physiologically active peptides have been isolated from it. This peptide inhibits the growth of, and may kill, bacteria, pref. gram negative bacteria. This peptide or its functional derivatives may be used in human or veterinary medicine for therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-bacterial polypeptide - active against Gram negative bacteria.
                                                                                                                                    Pig; small intestine; endocrine; gram negative; bacteria; therapeutic; veterinary medicine; prophylactic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 83; DB 2; Length 39; 100.0%; Pred. No. 0.0031; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Boman HG, Mutt V, Joernvall H;
              AAR30491 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 10; 15pp; English.
                                                                                                                                                                                                                                                           92WO-SE000394.
                                                                                                                                                                                                                                                                                     91SE-00001838.
                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100
Matches 14; Conservative
                                                                                                        Antibacterial peptide.
                                                                                                                                                                                                                                                                                                              (LEEJ/) LEE J.
(BOMA/) BOMAN H G.
(MUTT/) MUTT V.
(JOER/) JOERNVALL H.
                                                                                                                                                                            Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-018080/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39 AA;
                                                                                                                                                                                                       WO9222578-A1.
                                                                                                                                                                                                                                                           10-JUN-1992;
                                                                                                                                                                                                                                                                                     14-JUN-1991;
                                                                25-MAR-2003
12-MAY-1993
                                                                                                                                                                                                                                23-DEC-1992
                                        AAR30491;
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                                                                                                                                                                                                                                                                                                                                                                                 Lee J,
AAR30491
ID AAR3
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Search completed: October 26, 2005, 05:12:08 Job time : 55.1091 secs

1 RRRPRPPYLPRPRP 14 

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Gaps . 0

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OM protein - protein search, using sw model

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October 26, 2005, 05:00:14; Search time 10.4364 Seconds (without alignments) 129.071 Million cell updates/sec US-10-014-147-7 83 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RRRPRPPYLPRPRP 14 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	antimicrobial prot	bactenecin 7 - bov	antimicrobial pept	hypothetical prote	spore coat protein	hypothetical prote	protein-tyrosine-p	ω	hypothetical prote	n 14	Ω.			hypothetical prote	probable cytochrom	hypothetical XrepB	infected cell prot	glycoprotein D pre	protein R13D11.3 [	ferulate-5-hydroxy				ᆽ	hypothetical prote				Contract of the Contract of th
	Ω	868232	A36589	S68230	T29373	A41051	G86292	JC4155	JC2366	S76867	S35330	S14981	T33700	T22261	T29299	AC0665	S09612	WMBEXE	VGBE50	A88942	T04591	JQ1663	B48232	A48232	S55036	T13478	T32652	T35474	D96621	
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	Query Match Length	172	59	190	184	82	1006	1187	1189	192	168	199	210	218	589	134	139	261	402	437	520	301	196	209	258	359	427	456	665	
de.	Query Match	100.0	79.5	6.69	63.9	63.3	62.7	62.0	62.0	60.2	59.6	59.6		6.	٩.	57.8	57.8	57.8	57.8	57.8	57.8		9.95		56.6	56.6		9.99		
	Score	83	99	28	53	52.5	ıΛ	51.5	51.5	20	49.5	•	49	49	49	48	48	48	48	48	. 48	47.5	47	47	47	47	47	47	47	
	Result No.		8	'n	4	ď	9	7	00	σ	10	11	12	13	14	15	16	17	18	1.6	50	. 21	22	23	24	25	26	27	28	

ubiquitin-like fus hypothetical prote	Ca(2+)-sensing recribonucleoside-dip	proline-rich prote apidaecin Ib precu	apidaecin 22 precu hypothetical prote	PBDX protein - num cytochrome b(561) cytochrome b(561)	cytcchrome b561 - splicing factor RS splicing factor RS apidaecin 73 precu
JN0674 T46517	QQBEC3 S40476 G69457	T02436 S06675	S35331 C72501	S43791 B85737 G90881	E64893 T51304 T47978 S35332
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744	47 47 46.5	46.5	4 6 6	4 4 4 6 6 6	4 4 4 4 6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6
30	332	32 30 30	37 38	39 4 4 1 0	4 4 4 4 0 6 4 7

## ALIGNMENTS

	000011 1
	antimicrobial protein PR-39 precursor, cachellicassociaced - p-9 N,Alternate names: myeloid antibacterial protein PR-39
	C;Species: Sus scrofa domestica (domestic pig) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
	C,Accession: S68232; JN0899; I47138; S19563
	R,Zhao, C.; Ganz, T.; Lenrer, K.1. FEBS Lett. 376, 130-134, 1995
	A,Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni
	A;Kerefrence number: S08232; MOID:90103303; FMID:/130020 A:Accession: S68232
	A;Status: translation not shown
	A Nolecule type: DNA
	A; RESIGNES: 1-1/4 < 2.0.0.7.4. P.
	A) Experimental source: leukocytes
	K)SCOTIC1, F.; &SIECL1, M. K)SCOTIC1, F.; &SIECL1, M. S. Ochkon Biochive Dear Commun 196 1058-1065, 1993
	A, Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the
	A, Reference number: JN0899; MUID: 94071853; PMID: 8250863
	A A A COCESSION: UNUSAY A A A COCESSION: UNUSAY A A A COCESSION: UNUSAY A A A COCESSION: UNUSAY A A A A COCESSION: UNUSAY A A A A COCESSION: UNUSAY A A A A A COCESSION: UNUSAY A A A A A A A COCESSION: UNUSAY A A A A A A A A A A A A A A A A A A
	A;Residues: 1-20, A', 22-172 <sto></sto>
	A; Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101
	A; Experimental gource: bone marrow cells
	Rigudmindsbon, G.H.; Magnusson, K.F.; Chowminsbon, H.; Jouransbon, H.; Magnusson, E.; John J., Magnusson, E.; John J., Magnusson, E.; John J., Magnusson, H.; Magnusson, M.; John J., Marian
	FIGURATION NATURAL STIT. 0.3.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.
	A; Reference number: 147138; MUID:95350216; PMID:7624374
	A;Accession: 147138
	A;Status: preliminary; translated from GB/EmbL/UDBJ
	A;MOLECULE CYPE: DNA A:Desiding: 1-28 'T', 30-89', OR', 92-116', NDP', 120-172 <gud></gud>
	A. Cross-references: BMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298
	R; Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall
	Bur. J. Biochem. 202, 849-854, 1991
	AjTite: Annino acia Bequence or Ek-29. Isolataton 1100. A. Doferance number: 81968, MITD: 92111534; PMID:1756998
	A: Accession: S19563
_	A, Molecule type: protein
	A;Residues: 131-169 <age></age>
	A, Experimental source: intestine
	C;Genetics:
	A.Tutrone: 66/3: 102/3: 126/3
	C; Superfamily: cathelin; cystatin homology
	C; Keywords: amidated carboxyl end; antibacterial
	F;1-29/Domain: signal Bequence #statub predicted <pre>c</pre>
	Figeral Domain: Operation Manager 7 vers.
	F;30-130/Domain: projecture moracus projectus experimental <mat></mat>
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Matches

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A; Residues: 'XX',3-11 (BOU)
A; Residues: 'XX',3-11 (BOU)
A; Residues: 'XX',3-11 (BOU)
A; Residues: 'XX',3-11 (BOU)
A; Residues: 'XX',3-11 (BOU)
A; Note: the material sequence strain JH642
A; Note: the material sequence of the transcription start site and peptide sequencing of the I R; Nunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berterr C; Broni, S; Brouillet, S; Bruschi, C.V, Caldwell, B.; Azidono, V; Carter, N.M.; Choi, A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerriech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Lardinois, A; Lardinois, A; Landors, E. A; Oudega, B.; Park, S.H.; Parko, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tognoni, A.; Tosto, V.; Uchiyama, T.; Winters, P.; Wippt, A.; Yanamoto, H.; Yanamoto, K.; Yata, K.; Yoshida, K.; Akuthors: Yoshikawa, H.; Danchin, A.; Asturbors: Experience of the Gram-Positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: part of this sequence, including the amino end of the mature protein, was confirm R; Bourne, N.; FitzJames, P.C.; Aronson, A.I.
J. Bacteriol. 173, 6618-6625, 1991
A; Title: Structural and germination defects of Bacillus subtilis spores with altered cont A; Reference number: A41051; MUID:92011439; PMID:1917883
                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:023291; EMBL:U55363; PIDN:AAA97967.1; GSPDB:GN00023; CESP:ZC:
A;Experimental source: strain Bristol N2; clone ZC404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spore coat protein precursor - Bacillus subtilis
Cispecies: Bacillus subtilis
Cipate: 01-Apr-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
CiAccession: 804835; A41051; F69606
RiAronson, A.I.; Song, H.Y.; Bourne, N.
A.M. Microbiol. 3, 437-444, 1989
A;Title: Gene structure and precursor processing of a novel Bacillus subtilis spore coat
A;Reference number: 804835; MUID:89313296; PMID:2546006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 'MNVHTPNLSIRNMVKGIKKAREVFLL',2-82 <AR2>
A,Cross-references: UNIPROT:P11863; EMBL:X13740; NID:g39864; PIDN:CAA32004.1; PID:g39865
A,Experimental source: strain JH642
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A;Cross-references: GB:299110; GB:AL009126; NID:g2633472; PIDN:CAB13066.1; PID:g2633563
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 5
A;Introns: 15/2; 50/2; 75/2; 138/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC404.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                               submitted to the EMBL Data Library, April 1996
A; Description: The sequence of C. elegans cosmid ZC404.
A; Reference number: 220614
                                                                                                                                                                A,Status: preliminary; translated from GB/EMBL/DDBJA,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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0; Mismatches
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Best Local Similarity 90.00,
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                                                                                                                                                                                                                                         A; Residues: 1-184 <BEN>
                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: ZC404.1
                                                                                                                                    A; Accession: T29373
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G
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C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form following
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C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C,Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Ç;Accession: T29373
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F:29-130/Domain: propeptide #status predicted <PRO>
F:130-190/Product: antimicrobial peptide #status predicted <MAT>
                                                                  Length 172;
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Pred. No. 1.1;
0; Mismatches 3; Indels
                                                                                                                                    0; Indels
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FEBS Lett. 376, 225-228, 1995
A;Title: cDNA sequences of three sheep myeloid cathelicidins.
A;Reference number: S68228; MUID:96105386; PMID:7498547
A;Accession: S68230
                                                              100.0%; Score 83; DB 2; 1
100.0%; Pred. No. 0.00066;
tive 0; Mismatches 0;
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Pred. No. 0.033;
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A,Molecule type: protein
A;Reaidues: 1-59 <FRA>
C;Superfamily: cathelin; cystatin homology
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78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                14; Conservative
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les 12; Conserva
                                                                  Query Match
Best Local Similarity
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A;Residues: 1-190 <BAG>
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Query Match Best Loca Matches

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A; Experimental source: thymus C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-bi C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase P; 3.102/Domain: protein 4.1 membrane-binding domain homology <841> P; 566-575/Region: prolline-rich P; 712-718/Region: acidic
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*Residues 1-192 «KAN»
A;Cross-references: UNIRROT:P74661; EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA1877:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse NiAlternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phos C;Species: Mus musculus (house mouse) C;Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: JC2366
R;Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.
Biochem: Bloghya: Res: Commun. 203, 479-484, 1994
A;Title: CDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskelet A;Reference number: JC2366; MUID:94354845; PMID:8074693
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Date: 25-Apr-1997
B; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, A.; Stubence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: JC2366
A;Molecule type: mRNA
A;Residues: 1-1189 <SAW>
A;Cross-references: UNIPROT:Q62130; GB:D31842; NID:g507330; PIDN:BAA06628.1; PID:g507331
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F;1123/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1129/Binding site: substrate phosphate (Arg) #status predicted
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41> F;566-575/Region: proline-rich F;709-716/Region: acidic F;719-716/Region: acidic F;913-1169/Domain: protein-tyrosine-phosphatase homology <PTP2> F;1121/Active site: Cys (phosphocysteine intermediate) #status predicted F;1121/Active site: cys (phosphate (Arg) #status predicted
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                                                                                                                                                                                                                          DB 1; Length 1187;
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Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51.5; DE Fred. No. 42; 0; Mismatches
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Pred. No. 42;
0; Mismatches
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83.3%;
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83.3%;
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69.2%;
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565 RPPPPY-PRPRP 575
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                3 RPRPPYLPRPRP 14
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A; Status: preliminary
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A;Map postiton: 1912.2-1912.2
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-t
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: G86292
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Yi, Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: G86292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1006 <STO>
A;Cross-references: UNIPROT:09LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN
C;Genetics:
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A,Molecule type: mRNA
A,Residues: 1-1187 <8ML>
A,Cross-references: UNIPROT:Q15678; EMBL:X82676; NID:g3929753; PIDN:CAA57993.1; PID:g809
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R;Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, Biochem Biophys. Res. Commun. 209, 959-965, 1995
Biochem Biophys. Res. Commun. 209, 959-965, 1995
A;Tile: PEZ:a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like A;Reference number: JC4155; MUID:95251727; PMID:7733990
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                         Comment: This structural protein is expressed during stage V of sporulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                           Keywords: sporulation
1-19/Domain: propeptide #status experimental <PRO>
:20-82/Product: spore coat protein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Arabidopsis thaliana
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Pred. No. 31;
0; Mismatches
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81.8%;
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83.3%;
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity
Matches 9; Conserva
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                                                                                     A;Gene: cotT
A;Start codon: TTG
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                                                            Genetics:
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A;Cross-references: UNIPROT:Q9GZE0; EMBL:AF100656; PIDN:AAC68952.1; GSPDB:GN00022; CESP:8
A;Experimental source: strain Bristol N2; clone F49F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-218 <WIL>
A;Cross-references: UNIPROT:001331; EMBL:Z81539; PIDN:CAB04391.1; GSPDB:GN00019; CESP:F46
A;Experimental source: clone F46A8
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C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
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A;Residues: 1-589 <10H>
A;Cross-references: UNIPROT:Q18756; EMBL:U41557; PIDN:AAA83307.1; CESP:C50F7.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22261
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Rimiller, N.; Wammeley, P. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid F49Fl. A;Reference number: Z21389 A;Accession: T33700 A;Accession: Type: Draiminary; translated from GB/EMBL/DDBJ A;Residues: 1-210 <ML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F46A8.5 - Caenorhabditis elegans
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Harris, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19539
A;Accession: T22261
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
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A; Introns: 130/3
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                                                                                                                                                                                                apidaecin 14 precursor - honeybee
N; Contains: apidaecin II
C; Species: Apis mellifera (honeybee)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C; Accession: S35330; S06676
C; Accession: S35330; S06676
C; Accession: S15330; S06676
A; Capaci, T.; Casteels, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1937
A; Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplificat
A; Reference number: S35330; MUID:93223697; PMID:8467807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-168 <CAS>
A; Cross-ternces: 1-168 <CAS>
A; Cross-ternces: UNIPROT: Q06601; EMBL: X72575; NID: 9297062; PIDN: CAA51167.1; PID: 92970
R; Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J. 8, 2387-2391, 1989
A; Title: Apidaecins: antibacterial peptides from honeybees.
A; Reference number: S05383; MUID: 90005446; PMID: 2676519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S14981
R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response A;Reference number: S14970; MUID:91329690; PMID:1714316
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C;Species: Lycopersicon esculentum (tomato)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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A;Remiduem: 43-60 <CA2.
C;Superfamily: procyclic acidic repetitive protein
F;43-60/Product: apidaecin II #statum experimental <MAT>
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A/Status: preliminary
A/Rolcoule Hype: mRNA
A/Rolcoule: 1-199 «SHO>
A/Cross-references: BMBL:X55692
A/Cross-references: EMBL:X55692
C/Superfamily: hydroxyproline-rich glycoprotein
C/Keywords: cell wall; glycoprotein; hydroxyproline
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                                                             3 RRPPPRYTPPRP 15
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        RRPRPPYLPRPRP
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Score 49; DB 2; Length 589;
Pred. No. 44;
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   Query Match 59.0%;
Best Local Similarity 81.8%;
Matches 9; Conservative (
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Accession: Salmonella enterica serovar Typic Species: Salmonella enterica serovar Typic Species: Salmonella enterica serovar Typic C; Species: Salmonella enterica serovar Typic C; Species: Salmonella enterica serovar Typic C; Species: Salmonella enterica serovar Typic A; Note: this species has also been called Salmonella typhic C; Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002 C; Accession: ACG65 R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova, A; Reference number: AB0502; MUID:21534947; PMID:11677608 A; Stetus: preliminary A; Molecule type: DNA A; Residues: 1-134 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD01692.1; PID:g16502543; GSPDB:GN00176 C; Genetics: A; Genetics: Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Genetics: A; Genetic

Gaps ., 0 Query Match 57.8%; Score 48; DB 2; Length 134; Best Local Similarity 63.6%; Pred. No. 14; Matches 7; Conservative 2; Mismatches 2; Indels

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4 PRPPYLPRPRP 14 | || :|||:| 25 PTPPIVPRPKP 35

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Search completed: October 26, 2005, 05:20:02 Job time: 11.4364 secs

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SEQUENCE FROM N.A.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AT17 HUMAN QBLNW3	P74661 Q8PHZ0 Q69260	Q7Z727 Q6JAF9 AP14 APIME	09FSP4 06EQW6 066852	Q96GV2 Q9GZE0	008306
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# ALIGNMENTS

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SECTENCE OF 131-164, AND FUNCTION.
TISSUE=Neutrophils;
MEDIJINE=55088504; PubMed=7996056;
Shi J., Ross C.R., Chengappa M.M., Blecha F.;
"Identification of a proline-arginine-rich antibacterial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99350216; PubMed=7624374; MEDLINE=99350216; PubMed=7624374; Chowdhary B.P., Johansson M., Gudmundson G.H., Magnusson K.P., Chowdhary B.P., Johansson M., Andersson L., Boman H.G.; "Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene family member: comparative mapping of the locus for the human peptide antibiotic PLL-39."; proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Intestine;
MEDLINE=92111534; PubMed=1765038;
Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
Mutt V.; Joenvall H.;
"Amino acid sequence of PR-39. Isolation from pig intestine of a new
member of the family of proline-arginine-rich antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
TISSUB-Bone marrow;
MEDLINE=94071853; PubMed=8250863;
Storici P., Zanetti M.;
N. Canetti M.;
A cuny derived from pig bone marrow cells predicts a sequence identical to the intestinal antibacterial peptide PR-39.";
Bjochem. Biophys. Res. Commun. 196:1058-1065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao C., Ganz T., Lehrer R.I.;
"Structures of genes for two cathelin-associated antimicrobial peptides: prophenin-2 and PR-39.";
PEBS Lett. 376:130-134(1995).
                              PRO054: Q9TR84;
01-MAR-1992 (Rel. 21, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Antibacterial protein PR-39 precursor.
172 AA
   PRT;
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                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
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MEDLINE=95010707; PubMed=7925973; DOI=10.1016/0014-5793(94)00954-6;
Scocchi M., Romeo D., Zanetti M.;
"Molecular cloning of Bac7, a proline- and arginine-rich antimicrobial
neutrophils that is analogous to PR-39, an antibacterial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
              the small intestine.";
J. Leukoc. Biol. 56:807-811(1994).
-1- FUNCTION: Exerts a potent antimicrobial activity against both
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Proline amide (G-170 provides amide
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Pyrrolidone carboxylic acid (By
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                                                                   E.COli and B.megaterium.
--- TISSUE SPECIFICITY: Small intestine and bone marrow.
--- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994B792798C0E133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G -> A (in Ref. 2).
A -> T (in Ref. 1).
RO -> OR (in Ref. 1).
IHS -> NDP (in Ref. 1).
P -> I (in Ref. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                            PRODOM; PRO0666; Cathelicidins; 1.
PRODOM; PRO01838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_2; 1.
Amidation; Antibiotic; Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
SIGNAL 1 29 Potential.
PROPEP 30 130 Antibacterial protein POD_RES 30 30 Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-UUL-2004 (Rel. 44, Last annotation update)
Bactenecin 7 precursor (BAC7) (PR-59).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group).
G -> A (
                                                                                                                                                                                                                                                                                                             EMBL, X87236, CAA60682.1; -.
EMBL, 123825; AAA31109.1; -.
EMBL, X89201; CAA64487.1; -.
EMBL, S68232, S68232.
HSSP, P32196; IKWI.
InterPro; IPR001894; Cathelicidin.
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157 157 E
172 AA; 19476 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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124
169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae, Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCT7 BOVIN
ID BCT7 BOVIN
AC P19661;
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DISULFID
MOD_RES
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CONFLICT
SEQUENCE
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SOTI THE FEET THE SOLUTION OF THE STATE OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE
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                                                                                                                                                                                                                                                                                                                                                                          Frank R.W., Gennaro R., Schneider K., Przybylski M., Romeo D.;
"Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of bovine neutrophils.";
J. Biol. Chem. 265:18871-18874(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Direct protein sequencing; Pyrrolidone carboxylic acid;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Removed partially.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                      Scocchi M., Wang S., Zanetti M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21567 MW; 8CD07D7AA30A731C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 AA.
                                                                                                                                                                  SEQUENCE OF 131-189, AND MASS SPECTROMETRY TISSUE=Neutrophils;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION, AND MASS SPECTROMETRY.
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peptide from bovine neutrophils.";
FEBS Lett. 352:197-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 142977, AAA87359.1; -.
EMBL, Y09471; CAA70616.1; -.
HSSP, P32196; LKWI.
INCEPTO; IPRO1894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                               PubMed=8706679;
                                                                                                                                                                                                              MEDLINE=91035404; PubMed=2229048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.7 nes 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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130
190
30
30
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189
30
85
107
190 AA;
                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96300243;
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                                                                                      rissum=Liver;
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190 AA
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7.5 kDa bactinecin (Fragment)
                                                                                                                                                                                                    antimicrobial peptide.";
FEBS Lett. 377:519-522(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 RLRPRRPRLPRPRP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                          Ovis aries (Sheep).
Eukaryota, Metazoa, C
Mammalia, Eutheria, C
Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                      SEQUENCE FROM N.A.
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                                                                                         NCBI_TaxID=9940;
                                                                                                                                        TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT7 SHEEP
P50415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence analysis of Streptomyces venezuelae bacteriophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (In) Unknown A. (eds.);
MICROBIAL IMMUNE EVASION STRATEGIES - MEETING OF THE BELGIAN SOCIETY
FOR MICROBIOLOGY, pp.30-30, Unknown publisher (2003).
                                                                                                                                                                                                                                                                                                                                                                                                        Van Mellaart L., Mei L., Lammertyn E., Schacht S., Anne J.; "Site-specific integration of bacteriophage VWB genome into Streptomyces venezuelae and construction of a VWB-based integrative
                                                                                                                                                                                                                                                                                                                Analysis of the open reading frames of the main capsid proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Van Dessel W., Van Mellaert L., Raasch C., Liesegang H., Streit W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an Dessel W., Van Mellaert L., Raasch C., Liesegang H., Streit W.,
                                                                                                                                          Anne J., Van Mellaert L., Decock B., Van Damme J., Van Aerschot A.,
Herdewijn P., Evssen H.:
                                Hypothetical protein.
Batceriophage WWB.
Viruses; dSDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                      Purther biological and molecular characterization of actinophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                  NEGUENCE FROM N.A.
MEDLINE=95336309; PubMed=7611876;
Anne J., Piten P., Van Mellaert L., Joris B., Opdenakker G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
71.1%; Score 59; DB 2; Length 166;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 12; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Mellaert L.M.G.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY320035, AAR29707.1; -...
Hypothetical protein.
SEQUENCE 166 AA, 18526 MW, 7FA9BE7F95888A9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
   27, Last sequence update)
27, Last annotation update)
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                                                                                                                                                                                                                      Gen. Microbiol. 136:1365-1372(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91037942; Pubmed=2230721;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99098696; PubMed=9884227;
                                                                                                                                                                                                                                                                                                                                                 Arch. Virol. 140:1033-1047(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 144:3351-3358(1998)
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    05-JUL-2004 (TrEMBLrel.
                     05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                actinophage VWB.";
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                                                                                                NCBI_TaxID=10702;
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Anne J.;

P79361; P79361

RESULT 4 P79361

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MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;

MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;

Bagella L., Scocchi M., Zanetti M.;

"cDA sequences of three sheep myeloid cathelicidins.";

FEBS Lett. 376:225-228(1995).

-:- FUNCTION: Exerts, in vitro, a potent antimicrobial activity.

Probably due to an impairment of the function of the respiratory probably due to an impairment of the function of the respiratory chain and of energy-dependent activities in the inner membrane of susceptible microorganisms (By similarity).

-:- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            MEDLINE-96140581; PubMed-8549789; DOI=10.1016/0014-5793(95)01390-3; Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.; "Molecular analysis of the sheep cathelin family reveals a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name=BAC7.5;
Ovis aries (Sheep).
Name=BAC7.5;
Ovis aries (Sheep).
Mammalia; Rutheria; Cetartiodactyla; Ruminantia; Botora; Bovidae; Caprinae; Ovis.
Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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GO; GO:000552; P:defense response; IEA.
GO; GO:000613; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00066; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Liver;
Huttner K.M., Mahoney M.M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 1060598, AAB49713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 AA; 18642 MW; E3BFC871F6AE8B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.9%; Score 58; DB 2; 78.6%; Pred. No. 5.3; vative 0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Created)
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                       PRT;
                 019031 PRELIMINARY;
019031;
01-JAN-1998 (TEMBLrel. 05,
01-JAN-1998 (TEMBLrel. 05,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 KLRPRRPRLPRPRP 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 78.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=9940;
                                                                                                                                                            Bactinecin 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q9RK54;
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019031
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005575; P:defense response; IEA.
GO; GO:0009613; P:defense to peet, pathogen or parasite; IEA.
GO; GO:0009613; P:response to peet, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidins; 1.
PRODOM; PD001894; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
                             or send an ema...

R EMBL; L46852; AAA85468.1; -..

PIN; S6230; S68230.

B RISP; P32196; 1KUN.

DR HSSP; P32196; 1KUN.

DR Prodom; P000683; Cathelicidin; 1.

DR Prodom; P0001838; Cathelicidin; 1.

DR PROSITE; PS00947; CATHELICIDINS 1; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

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DR PROSITE; PS00947; CATHELICIDINS 2; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

POPERATION 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

DR PROSITE; PS00947; CATHELICIDINS 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

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PS00947; CATHELICIDINS 2; 1.

PS00947; CATHELICIDINS 2; 1.

PS00947; CATHELICIDINS 2; 1.

PS00947; CATHELICIDINS 2; 1.

PS00947
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrrolidone carboxylic acid (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;
Zhao C., Nguyen T., Brogden K., Lehrer R.;
Submitted (UN11999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ243125; CAB45523.1; -.
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SEQUENCE 190 AA; 21835 MW; D13305EF16875F4F CRC64;
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By similarity.
E4AAFB1600E98371 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Bac7.5 protein.
Name-bac7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 AA
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ses 11; Conservative
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107
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STRAIN=A3(2) / M145,
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
MINIMARIAN TO CARROWN S., Cardeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Arnor D., Bateman A., Goble A., Hidalgo J., Hornby T., Howarth S.,
Traner A., Goble A., Hidalgo J., Hornby T., Hornby T., Rowarth S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                              Name-Bacll;
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
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Nature 417:141-147(2002).
EMBL; AL939105, CAB56128.1; -.
COMPLETE PIOCECOME; Hypothetical protein.
SEQUENCE 200 AA; 22076 MW; ODCBBEC5585803B5 CRC64;
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GO; GO:0006952; P:defense response; IEA.
GO; GO:00069613; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
Pfon666; Cathelicidins; 1.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycese, Strepto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huttner K.M., Mahoney M.M.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U77049; AAB62000.1; -..
EMBL; U77046; AAB62000.1; JOINED.
EMBL; U77047; AAB62000.1; JOINED.
EMBL; U77048; AAB62000.1; JOINED.
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PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
SEQUENCE 224 AA, 25669 MW; GAEAAB1256AC76FC CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein SC00323.
ORFWames=SCF12.02;
                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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224 AA
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Gramene; Q7XTY0;
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                                                                                     RESULT 11
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBL_TAXID=39947;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003888; BAD115681.;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
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MEDLINE=22885473; PubMed=14523113; DOI=10.1099/mic.0.26528-0;
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1764;
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66.3%; Score 55; DB 2; Length 337;

Best Local Similarity 76.9%; Pred. No. 27;

Matches 10; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eckstein T.M., Belisle J.T., Inamine J.M.;
"Proposed pathway for the biosynthesis of serovar-specific glycopeptidolipids in Mycobacterium avium serovar 2.";
Microbiology 149:279-2807 (2003).
EMBL; AR14372; AAD44199.1; -...
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Pred. No. 16;
Score 57; DB 2; Length 200;
Pred. No. 8.8;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative amino acid permease.
                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAV-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
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Best Local Similarity 71.4%;
Matches 10; Conservative
    68.7%;
76.9%;
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      Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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Q9XCG4
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Pubmed=12444439; DOI=10.1018/nature01183; Frag Y., Li Y., Zhu J., Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Yinng K., Yu S., Tang Y., Liu Y., Hu X., Lu T., Li W. Y., Wu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Lv G., Gu W., Zhu G., Yu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Toledo;
MEDLINE=9609916; PubMed=8523595;
MEDLINE=9609941, Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
"Human cytomegalovirus clinical isolates carry at least 19 genes not found in laboratory strains.";
J. Virol. 70:78-83(1996).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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65.1%; Score 54; DB 2; Length 336;
Best Local Similarity 76.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 3; Indels
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 336 AA; 35116 MW; 9F865E5019F69D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus.
Viruses; daDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OSJNBAO019KO4.17 procein.
Name-OSJNBAO019KO4.17;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 AA.
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EMBL; AL606640; CAD41670.3; -.
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                                          320 RRPRPPALPPPP 332
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2 RRPRPPYLPRPRP 14
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Streptomyces avermitilis.
                                            SEQUENCE FROM N.A. STRAIN=MA-4680;
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                                                                                                                      metabolites.";
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                  DB 2; Length 397;
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                                     1; Indels
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase; WBGene00022601; ZC404.1.
Wormbep; ZC404.1; CB07592.
Hypotheilal protein.
SEQUENCE 184 AA; 21649 MW; 6D64D09EA91308F9 CRC64;
BAFC545CBFA4EB22 CRC64;
                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein 25(404.1.)
Name=2C404.1; ORFNames=ZC404.1;
Caenorhabditis elegans.
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Last annotation update)
                 Score 53.5; DB; Pred. No. 50; 0; Mismatches
                                                                                                                       184 AA.
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MEDLINE=99069613; PubMed=9851916;
43737 MW;
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EMBL; US5363; AAA97967.1; -.
PIR; T29373; T29373.
                  64.5%;
84.6%;
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01-JUN-2003 (TrEMBLrel. 24,
01-MR-2004 (TrEMBLrel. 26,
Hypotherical protein
OrderedLocusNames=SAV725;
                                                      2 RRPRPPYLPRPRP 14
                                                                  11; Conservative
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                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
Bentley D., Le T.T.;
"The sequence of C. e
                                                                                                                                                                                                                                                                                                                                                                                                                                   WormBase Consortium;
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Best Local Similarity
397 AA;
                  Query Match
Best Local Similarity
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SEQUENCE
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Matches
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connective tissue.
--- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II.
--- SUBCELLUTAR LOCATION Secreted, extracellular matrix.
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Nat. Biotechnol. 21.526-531(2003).
EMBL; AP005023; BAC68435.1;
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"The leucine-rich repeat protein PRELP binds perlecan and collagens and may function as a basement membrane anchor.";
and may function as a basement membrane anchor.";
J. Biol. Chem. 277:15061-15068 (2002).
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MEDLINE=20576219, Pubmed=11007795; DOI=10.1074/jbc.M007917200;
MEDLINE=20576219, Pubmed=11007795; DOI=10.1074/jbc.M007917200;
Bengtason E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D.;
"The amino-terminal part of PRELP binds to heparin and heparan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
Se FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last amotation update)
Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                            MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=33903;
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SEQUENCE 273 AA; 29246 MW; FE024904356085C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.9%; Score 53; DB 2; 71.4%; Pred. No. 39; Live 0; Mismatches
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J. Biol. Chem. 275:40695-40702(2000).
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 RRRPRPPARPGSRP 237
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Matches 10; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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-!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain.
-!- SIMILARITY: Belongs to the small leucine-rich proteoglycan (SLRP) family. Class II subfamily.
-!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                           EMBL; AF163568; AAG23723.1; -.
HSSP; P25146; 106S.
InterPro; IPR001611; LRR.
InterPro; IPR001372; LRR. LYP.
Pfam; PF00560; LRR; 11.
Pfam; PF00560; LRR; 11.
PRINTS; PR00019; LENRYT; 1.
SMART; SM00013; LRRWT; 1.
Extracellular matrix; Glycoprotein; Leucine-rich repeat; Repeat;
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(GlcNAc. .) (Potential).
(GlcNAc. .) (Potential).
(GlcNAc. .) (Potential).
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23DA99C01BB772A0 CRC64;
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Poly-Leu.
By similarity.
N-linked (GlCNA
N-linked (GlCNA
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Pred. No. 55;
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Prolargin.
Cys-rich.
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ilarity 76.9%;
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Matches 10; Conserva
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DISULFID
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Search completed: October 26, 2005, 05:18:40 Job time : 51.4909 secs

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Sequence 21389,
Sequence 24767,
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                                                                                                                                                                                                  October 26, 2005, 05:02:04; Search time 14.3818 Seconds (without alignments) 72.667 Million cell updates/sec
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Sequence 163,
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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PCT-US95-12080-1
US-08-930-777A-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 24254, A Sequence 29164, A Sequence 19784, A Sequence 31878, A Sequence 24900, A Sequence 11819, A Sequence 21189, A Sequence 26133, A Sequence 26133, A Sequence 26133, A Sequence 26188, A Sequence 26133, A Sequence 26133, A Sequence 26133, A	Sequence 17338, A Sequence 17338, A Sequence 22406, A Patent No. 5470718 Patent No. 5470718
US-09-252-991A-24254 US-09-252-991A-29164 US-09-252-991A-19784 US-09-252-991A-32675 US-09-252-991A-3468 US-09-252-991A-34868 US-09-252-991A-1864 US-09-252-991A-1919 US-09-252-991A-31919 US-09-252-991A-31919 US-09-252-991A-3919 US-09-252-991A-29133 US-09-252-991A-29133 US-09-252-991A-29133	US-09-902-540-12987 US-09-252-991A-17338 US-09-252-991A-22406 5470718-4
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### ALIGNMENTS

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Floppy disk
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TYPE: amino acid
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MOLECULE TYPE: peptide
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MEDIUM TYPE:
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| Sequence 4, Application US/08930777A |
| Patent No. 6713605 |
| GENERAL INFORMATION: |
| APPLICANT: Blecha, Frank |
| APPLICANT: Blecha, Synthetic Antimicrobial Peptide |
| TITLE OF INVENTION: Synthetic Antimicrobial Peptide |
| TITLE OF INVENTION: Synthetic Antimicrobial Peptide |
| TITLE OF INVENTION: Synthetic Antimicrobial Peptide |
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| TITLE OF INVENTION: Synthetic Antimicrobial Peptide |
| TITLE OF INVENTION: Synthetic Antimicr
                                                                                                                                                                                                                                                                                                                       APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

CLASSIPICATION: 530

PRIOR APPLICATION: DATA:

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLII 10, 1996

CLASSIPICATION: 530

ATTORNEY/AGENT INFORMATION:

NAMME: COllins, John M.

REGISTRATION NUMBER: 23,525

REFERENCE/DOCKET NUMBER: 23,525

TELERPHONE: (816) 474-9057

INFORMATION FROM FILON:

CENTRANCE (READENTOR)

TELERPAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 7:

CENTRANCE CHARANCHERIESE
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                                                                                                                                                                                                  Sequence 7, Application US/08930777A Patent No. 6713605
GENERAL INFORMATION:
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1 RRRPRPPYLPRPRP 14
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Best Local Similarity 100.
Matches 14; Conservative
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GY: linear
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                                                                                                                         RESULT 2
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COMPATING SYSTEM: TIPM FOR COMPASSIONS
OSPERATING SYSTEM: PC-DOS/MS-DOS
OSPERATING NUMBER: US/08/30.777A
PRIGHOMATIC NUMBER: US/08/30.777A
PRIGHOMATIC NUMBER: 23.00, 399
PRIGHOMATIC NUMBER: 23.00, 399
PRIGHOMATIC NUMBER: 23.25.A
PRESIDENCE CONCERNING NUMBER: 23.25.A
PRESIDENCE CONCERNING NUMBER: 23.25.A
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PRESIDENCE CONCERNING NUMBER: 23.25.A
PRESIDENCE CONCERNING NUMBER: 23.25.A
PRESIDENCE CONCERNING NUMBER: 25.25.A
PRESIDENCE CONCERN
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US-08-930-777A-2
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                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sequence 2, Application US/09024975;
Patent No. 6133233
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: SHI, JISHU
APPLICANT: SHI, JISHU
APPLICANT: SHI, JISHU
APPLICANT: SHI, JISHU
APPLICANT: SHI, JISHU
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APPLICANT: SHI, JISHU
APPLICANT: SHI, JISHU
APPLICANT: SHI, JISHU
APPLICANT: NUMBER OF SEQUENCES:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
CONTRACTOR OF APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPL
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                                                                                                                                                                                                                                                                                  Length 26;
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                                                                                                                                                                                                                                                                                      Score 83; DB 2;
Pred. No. 0.00031;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
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                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                   ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 14; Conservative
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STRANDEDNESS: single
                              TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
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US-09-024-975-2
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; Sequence 2, Application US/08930777A

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US-09-739-535-1
US-09-739-535
; Sequence 1, Application US/09739535
; Patent No. 6794490
; GENERAL INFORMATION:
    APPLICANT: Cubiet Pharmaceuticals, Inc.
    TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; CURRENT PELLING NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 38
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100.0%; Score 83; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
ADDRESSEE: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
STATE: Missouri
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy disk
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION DATE: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION: DATE: April 10, 1996
CLASSIFICATION: JOHN M.
REGISTRATION: JOHN M.
REGISTRATION NUMBER: 230
ATTORNEY/AGENT NUMBER: 23625-A
TELEPHONE: A149050
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100.0%; Pred. No. 0.00045;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.º
Matches 14; Conservative
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TYPE: amino acid
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1 RRRPRPPYLPRPRP 14
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Mutt, Viktor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO PUBLICATION INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                            CILL.
STATE: GEC.
COUNTRY: USA
T9: 30309-4530
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AUTHORS:
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'Sequence 1, Application US/08310722

'Patent No. 5654273

'GENERAL INFORMATION:

APPLICANT: Gallo, Richard L.

APPLICANT: Klagsbrun, Michael

'TITLE OF INVERTION: Synducin Mediated Modulation of Tissue Repair

NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                     GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: BOMAN, Hans G
APPLICANT: BOMAN, Hans G
APPLICANT: BOMAN, Hans G
APPLICANT: MUTT, Viktor
APPLICANT: MOTT, Viktor
APPLICANT: JORNVALL, Hans
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.O. BOX 1404
CITY: Alexandria
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: LBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR DATE: 33-DEC-1992
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 33-DEC-1992
APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
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FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NUMBER: MO 92-22578
FILING DATE: APPLICATION NU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,113
FR: 003300-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 00330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                          US-08-162-052-1; Sequence 1, Application US/08162052; Patent No. 5489575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                               1 RRRPRPPYLPRPRP 14
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hovey, Williams, Timmons
                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE: 22-SEP-1994

CLASSIFICATION NUMBER: US/08/310,722

FILING DATE: 22-SEP-1994

ATTORNEY AGENT INFORMATION:

NAME: Pabet, Patrea L.

REGISTRATION NUMBER: CMC379

TELEPAN: (404)-815-6555

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acid

TYPE: amino acid

TYPE: ADDIOSY: Innear Home charing
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Patent No. 5830993
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: John M. Collins, Hovey, Williams, Timm
ADDRESSEE: Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Jornvall, Hans
AUTHORS: No. 5654273el Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2405 Grand Boulevard, Suite 400 CITY: Kansas City STATE: Missouri COUNTRY: U.S.A.

ZIP: 64108
COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: PLOSS SOFTWARE: Patentin Release #1.0, Version #
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
```

Gaps

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Sequence 1, Application US/09024975
; Sequence 1, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: SHI, JISHU
TITLE OF INVENTYON: PEPTIDE MODULATION OF REPERFUSION INJURY
INVERSE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE:
CONTRIBUTE OF COLLINS
STREET: MO.
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                                                                                                                                                                                                                                                                     Query Match . 100.0%; Score 83; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indele
                                                                                                AUTHORS: Mutt, Viktor
MUTHORS: Jornvall, Hans
TITLE: No. 5863897el Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-728-333-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/024,975 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
APPLING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLING, JOHN M.
REFERENCE/DOCKET NUMBER: 25.262
REFERENCE/DOCKET NUMBER: 25585-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
                                                         Lee, Jong-Youn
Boman, Hans G.
Mutt, Viktor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RRRPRPPYLPRPRP 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-024-975-1
                ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Yo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-024-975-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08728333
Patent No. 5863897
GENERAL INFORMATION:
APPLICANT: Gallo, Richard L.
APPLICANT: Klagsbrun, Michael
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 83; DB 2; Length 39; 100.0%; Pred. No. 0.00046; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 30109-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 Peachtree Street, Suite 2800
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,722
FILING DATE: 22-5EP-1994
ATTORNEY/AGENT INFORMATION:
                                  FILING DATE:
CLASSIFICATION: 530
ATTORNEY, FAGENT INFORMATION:
NAME: COLLING, JOHN M.
REGISTRATION NUMBER: 26262
REFERENCE DOCKET NUMBER: 2362F
TELECOMMUNICATION INFORMATION:
TELEPAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acide TOPOLOGY: 1.
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FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRRPRPPYLPRPRP 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-419-066-1
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REPERENCE/DOCKET NUMBER: 26,262
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-12080-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-930-777A-3
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GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporaton
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES:
ACORRESPONDENCE ADDRESS:
ADDRESSES: Patrea I. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 83; DB 4; Length 39; 100.0%; Pred. No. 0.00046; Live 0; Mismatches 0; Indels
        Sequence 1,74pplication US/08930777A
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent No. 6713605
Patent Shi, Jishu
PapelCANT: Shi, Jishu
PapelCANT: Shi, Jishu
PapelCANT: Shi, Jishu
PapelCANT: Shi, Jishu
PapelCANT: Shi, Jishu
PapelCANT: Shi, Jishu
PapelCANT: Showey, Williams, Timmons & Collins
CORRESPENT: Also Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Dispersion Processed
Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATIONS YSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
CLASSIFICATION S30
ATYONEY/AGENT INFORMATION:
NAME: Colling. John M.
REGISTRATION NUMBER: 25,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (816) 474-9050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRAACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RRRPRPPYLPRPRP 14
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
STATE: Georgia
COUNTX: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-08-930-777A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CT-US95-12080-1
-08-930-777A-1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08930777A
Patent No. 6713605
GENERAL INFORMATION
GENERAL INFORMATION
Frank
PAPLICANT: Blecha, Frank
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk

COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PATENTIN BATOR
FILING DATE: APPLICATION NUMBER: US/08/930,777A
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APPILION: S30
RIOR APPLICATION NUMBER: PCT/US96/04674
FILING DATE: APPILION: S30
CLASSIFICATION: S30
CLASSIFICATION: S30
CLASSIFICATION: S30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 83; DB 5; I Best Local Similarity 100.0%; Pred. No. 0.00046; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: Jornvall, Hans
IITLE: Novel Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
                                                                                  FILING DATE:
CLASSIFICATION:
TELECOMONICATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FINGHAL 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       S: Lee, Jong-Youn
S: Boman, Hans G.
S: Mutt, Viktor
S: Jornvall, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRPRPPYLPRPRP 14
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: anino acids
; TYPE: anino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide
; SCORE 68; DB 4; Length 23;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps
```

Search completed: October 26, 2005, 05:22:00 Job time : 15.3818 sec8

8 8

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; Search time 51.6727 Seconds (without alignments) 113.119 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/NSO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1862994 segs, 417510619 residues
                                                                                                                                                                                                                October 26, 2005, 05:05:05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                         US-10-014-147-7
83
                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                 OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Sequence 7, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli
	σī	US-10-014-147-7	US-10-651-147-7	US-10-391-155-3	US-10-014-147-4	US-10-651-147-4	US-10-014-147-2	US-10-651-147-2	US-09-738-742-1	US-09-739-535-1	US-10-014-147-1	US-10-391-155-1
	Query Match Length DB	14 14	14 15	15 15	19 14	19 15	26 14	26 15	38 9	38 9	39 14	39 15
de	Query Match 1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	83	83	83	83	83	83	83	83	83	83	83
	Result No.		7	e	4	v	9	7	60	σ	10	11

7	Sequence 6, Appli	'n	18,	14,	44,	20	'n		163	51,	e 16	5	89	-	4	'n	34		54214				2068	e 79,	4906	ednence		Sequence 134743,	20676	_	8	Sequence 114067,	Sequence 131115,
5 US-10-391-155-2	5 US-10-391-155-6	US-10-651-1		7 US-10-916-1	8	0 US-11-004-379-	4 US-10-014-147-3	ß	US-09-030-619	US-09-912-	5 US-10-277-232	5 US-10-277	US-10-838	US-10-344-70	US-10-391-1	US-10-502-639-	US-10-425	US-10-475-403	6 US-10-767-701-54214	US-10-437-96	US-10-425	-425-11	US-10-425-115-2	US-09-758-75		US-10-437-96	US-10-425-115-	10-437-963-	US-10-425-1	ns	US-10-437-963-1600	US-10-437-963-1	
39 1	39 1	-	٦	٦	٦	~	-	-		59			59 1	60	11 1	11 1	234 1	11 1	109 1	138 1	179 1	243 1	245 1	692 1	45 9	53 1	75 1	179 1	200 1	225 1	388 1	163 1	208 1
83 100.0	3 100	_		_	_	83 100.0	m	8 81.	6 79.	6 79.	6 79.	6 79.	6 79	79.	77.	4 77.	S	59 71.	58 69.9	6 67.	6 67.	6 67.	6 67.	56 67.5	5 66.	5 66.	5 66.	.99	5 66.	5 66.	5 66.	4 65.	4 65.
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	50	30	31	3.2	33	34	35	36	37	38	39	40	41	42	4.3	44	45

## ALIGNMENTS

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RESULT 1

US-10-014-147-7

Sequence 7, Application US/10014147

Publication No. US20030125249A1

Publication No. US20030125249A1

Publication No. US20030125249A1

Shi, Jishu

TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City
STATE: Missouri
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ON-Dec-2001

CLASSIFICATION NUMBER: US/10/014,147

FILING DATE: Ot-Dec-2001

PRIOR APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

FILING DATE: October 8, 1997

FILING DATE: APPLI 10, 1996

ATTORNEY/AGENT INFORMATION:
NAME: COLIINS, John M.
REGIERRICE/DOCKET NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 26,262
```

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1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-014-147-4
                                                                             US-10-391-155-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                          RESULT 3
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                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                      100.0%; Score 83; DB 14; Length 14; 100.0%; Pred. No. 0.0035; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION S30
PRIOR APPLICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/USS6/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELEPHONE: (816) 474.9950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 83; DB 15; Length 14; 100.0%; Pred. No. 0.0035; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
  ; TELEPHONE: (816) 474-9050
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; TYPE: amino acids
; TYPE: amino acid
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-014-147-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (816) 474-9057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                         1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                               1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRRPRPPYLPRPRP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                        Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-651-147-7
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                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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                                                                              AFFLICANT. Gao, Youne
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 83; DB 15; Length 15; 100.0%; Pred. No. 0.0037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10014147

Publication No. US20030125249A1

GENERAL INFORMATION:

APPLICANT: Blecha, Frank

TITLE OF INVENTION: Synthetic Antimicrobial Peptide

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hovey, Williams, Timmons & Collins

STREET: 2405 Grand Blvd., Ste. 400

CITY: Kansas City

STATE: Missouri

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE. Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC
OPERATING SYSTEM: MS XP
SOFTWARE: WordPerfect version 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BIS-044/D
TELECOMMUNICATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/391,155
FILING DATE: 18 Mar-2003
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 64108
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
Sequence 3, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                     APPLICANT: Simons, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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Gaps

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                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 9, 1997
APPLICATION NUMBER: PCT/USS6/04674
FILING DATE: April 10, 1996
ATTORNEY/AGNT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                      TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-651-147-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 26 amino acids
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                          SEQUENCE CHARACTERISTICS
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRRPRPPYLPRPRP 14
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Best Local Similarity 100.
Matches 14; Conservative
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100.0%; Score 83; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 14; Conservative 0; Mismatches 0; Indels
                        CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/10/014,147

FILING DATE: 07-Dec-2001

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/930,777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLICATION

NUMBER: PCT/US96/04674

FILING DATE: APPLI 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: COllins, John M.

REFERENCE/DOCKET NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELEPHONE: (816) 474-9950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-651-147-4
Sequence 4, Application US/10651147
Sequence 1, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City CITY: Missouri COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

PRILING DATE: October 8, 1997

RELING DATE: October 8, 1997

APPLICATION NUMBER: CT/US96/04674

FILING DATE: April 10, 1996

ATTORNEY AGENT INFORMATION:

NAME: COllins, John M.

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/651,147
FILING DATE: 28-AUG-2003
CLASSIFICATION: 530
              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (816) 474-9057
                                                                                                                                                                                                                                                                                                                                                                                                    (816) 474-9057
                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-014-147-4
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Sequence 1. Application US/09739535;
Publication No. US20020058785A1;
GENERAL INFORMATION:
APPLICANT: Cubist Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS;
FILE REFERENCE: C060
CURRENT APPLICANTON NUMBER: US/09/739,535;
CURRENT FILING DATE: 2000-12-15;
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
: LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 83; DB 9; Length 38; Best Local Similarity 100.0%; Pred. No. 0.0082; Matches 14; Conservative 0; Mismatches 0; Indels
                                       100.0%; Score 83; DB 9; Length 38; 100.0%; Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF NEWTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGBNI TINFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
                                                                                    0; Mismatches
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ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic US-09-739-535-1
                                                                                                                                        1 RRRPRPPYLPRPRP 14
                                                                                                                                                                    1 RRRPRPPYLPRPRP 14
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-014-147-1
US-09-738-742-1
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Publication No. US20020025924A1
GENERAL INPOWEMATION:
TITLE OF INVENTION:
FILE REFERENCE: C060
CURRENT APPLICATION NUMBER: US/09/738,742
CURRENT APPLICATION NUMBER: US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
SOFTWARE: PATENT OF US/09/738,742
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                              CUREUTER: FLORY disk
COMPUTER: TOPPY disk
COMPUTER: IBM PC compatible
COREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/651,147
FILING DATE: 28-Aug-2003
CLASSIFICATION NUMBER: US/08/930,777A
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISCRATON NUMBER: 26,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 83; DB 15; Length 26;
100.0%; Pred. No. 0.006;
trive 0; Mismatches 0; Indels
                                     Sequence 2, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howey, Williams, Timmons & Collins
STRET: 2405 Grand Blvd., Ste. 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (816) 474-9057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (816) 474-1 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                    ZIP: 64108
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                       STATE: Missouri
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 14; Conserve
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ORGANISM: Artificial
FEATURE:
                      US-10-651-147-2
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US-09-738-742-1
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US-10-391-155-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell De COMPUTER: Mordberfect version 10

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/10/391,155

FILING DATE: 18-Mar-2003

CLASSIFICATION: UNKNOWN

ATTORNEY AGENT INFORMATION:

NAME: DAVIG PRABANER: 29,693

REGISTRATION NUMBER: 29,693

REGISTRATION NUMBER: BEG.
                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 83; DB 14; Length 39; Best Local Similarity 100.0%; Pred. No. 0.0084; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 83; DB 15; Length 39; 100.0%; Pred. No. 0.0084; tive 0; Mismatches 0; Indels
REFERENCE/DOCKET NUMBER: 23625-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-391-155-1
                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-10-391-155-1
; Sequence 1, Application US/10391155
; Publication No. US2004009463A1
; GENERAL INFORMATION:
APPLICANT: Simons, Michael
Gao, Youhe
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 39 amino acids
                                                                                                                         LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRRPRPPYLPRPRP 14
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                               US-10-014-147-1
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Publication No. US20040009463A1
GENERAL INFORMATION: Michael
APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION: Method for PR-39 peptide mediated
selective inhibition of IKBA degradation
NUMBER OF SEQUENCES: 6
Sequence 2, Application US/10391155
Publication No. US20040009463A1
GENERAL INFORMATION:
APPLICANT: Simons, Michael
Gao, Youhe
TITLE OF INVENTION:
Belective inhibition of IKBA degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER EADABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC
COMPUTER: Dell PC
COMPUTER: Dell PC
COMPUTER: Dell PC
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COMPUTER: Dell PC
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100.0%; Pred. No. 0.0084;
Live 0; Mismatches 0;
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OPERATING SYSTEM: MS XP
SOFTWARE: WordPerfect version 10
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ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
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ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
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STATE: Massachusetts
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COUNTRY: USA
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COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 14; Conservative
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 28 - 440g - 2003

CLASSIFICATION DATA:

RAPPLICATION DATA:

RAPPLICATION DATA:

APPLICATION NUMBER: US/08/930, 777A

FILING DATE: October 8, 1997

APPLICATION NUMBER: PCT/US96/04674

FILING DATE: APPLI 10, 1996

ATTORNEY/AGENT INFORMATION:

NAME: COllins, John M.

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10651147
Publication No. US20040043934A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
Shi, Jishu
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Ste. 400 CITY: Kansas City TATE: Missouri COUNTRY: U.S.A.
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION UNDHER: 29,693
REFERENCE/DOCKET NUMBER: BIS-044/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                     APPLICATION NUMBER: US/10/391,155 FILING DATE: 18-Mar-2003 CLASSIFICATION: Unknown
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TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
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Matches
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Sequence 18, Application US/10344709C

| Sequence 18, Application US/10344709C
| Publication No. US20040170642A1
| GENERAL INFORMATION:
| APPLICANT: JORG FRITZ ET AL.
| TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin |
| TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin |
| TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin |
| TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin |
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| TITLE OF INVENTION: Vaccine which comprises at least one action and a cathelicidin |
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| TITLE OF INVENTION: Vaccine which comprises at least to a cathelicidin |
| TITLE OF INVENTION: Vaccine which comprises at
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, OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide US-10-344-709C-18
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels
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